

Db 559 AATACTGAAATGCACTTGTGCTAGACATGCTAAGATTAAGAAAGTAGCATGGAG 618
Qy 301 ATCTATATATATTTGGTACTCTTTAGTACTATTTGATGTAAGAGCCCTACACTT 360
Db 619 ATCTATATATATTTGGTACTCTTTAGTACTATTTGATGTAAGAGAGCCCTACACTT 678
Qy 361 GCCCATGCCAGCCCTAATGTCGGGTGACATGATTTGAGCCAGTACTATGATTAATTTACT 420
Db 679 GCCCATGCCAGCCCTAATGTCGGGTGACATGATTTGAGCCAGTACTATGATTAATTTACT 738
Qy 421 CTATGTTCTCTTTTGTAGTGTGTATTAAGATGTCCTTTTGTAGCCACTCGAGAG 480
Db 739 CTATGTTCTCTTTTGTAGTGTGTATTAAGATGTCCTTTTGTAGCCACTCGAGAG 798
Qy 481 ATCTTACTTAACTCTAGTGGCAATGATTTGAGCTCTGAGTCAACGCAATGCTCTGT 540
Db 799 ATCTTACTTAACTCTAGTGGCAATGATTTGAGCTCTGAGTCAACGCAATGCTCTGT 858
Qy 541 AATCTACTGACCACTACTCTGAGTGTGTCTTAACTTAACTATTCACGCTGCT 600
Db 859 AATCTACTGACCACTACTCTGAGTGTGTCTTAACTTAACTATTCACGCTGCT 918
Qy 601 AGTAATTACCAATCATTTTACAACACTGTTCATGTGTAGGGCTGC 645
Db 919 AGTAATTACCAATCATTTTACAACACTGTTCATGTGTAGGGCTGC 963

RESULT 2

US-10-759-602-1
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Paredy, Dayakar
Petolino, Joseph F.
Smith, Kelley
Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: DowAgrosciences LLC
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/759,602
FILING DATE: 16-Jan-2004
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 5110
TELEFAX: 317 337 4847
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-759-602-1

Query Match 100.0%; Score 645; DB 7; Length 6550;
Best local similarity 100.0%; Pred. No. 5,3e-164;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCAAGGTTCAATTCGCTCTCTGTATGTTCTTATATTAACGCTGACAAAGCT 60
|||||

Db 4420 GTCAAGGTTCAATTCGCTCTCTGTATGTTCTTATATTAACGCTGACAAAGCT 4479
Qy 61 ATAAAGCTTGATATGCACTATATATTAACAAGTTAGTACACAAGTTTGTACTTCAAG 120
Db 4480 ATAAAGCTTGATATGCACTATATATTAACAAGTTAGTACACAAGTTTGTACTTCAAG 4539
Qy 121 TCTTTTAACTATATGTTGGTGTGCAATTAAGTTATGAGTAATCCATATGAAGGTGTGCAAG 180
Db 4540 TCTTTTAACTATATGTTGGTGTGCAATTAAGTTATGAGTAATCCATATGAAGGTGTGCAAG 4599
Qy 181 AGAACATGAAGGCAAGAAAGATTAACGGAATGAAACCATTAAGCTTGGCTGTACAGCC 240
Db 4600 AGAACATGAAGGCAAGAAAGATTAACGGAATGAAACCATTAAGCTTGGCTGTACAGCC 4659
Qy 241 AATACTTGAATATGCACTTGTGTAGCATGCTTAAGTATTTAGAAAGATAGCATGGAGAG 300
Db 4660 AATACTTGAATATGCACTTGTGTAGCATGCTTAAGTATTTAGAAAGATAGCATGGAGAG 4719
Qy 301 ATCTATATATATTTGGCTAATCTTTAGTACTATTAATTTGATGAAAGCTTACACTT 360
Db 4720 ATCTATATATATTTGGCTAATCTTTAGTACTATTAATTTGATGAAAGCTTACACTT 4779
Qy 361 GCCCATGCCAGCCCTAATGTCGGGTGACATGATTTGAGCCAGTACTATGATTAATTTACT 420
Db 4780 GCCCATGCCAGCCCTAATGTCGGGTGACATGATTTGAGCCAGTACTATGATTAATTTACT 4839
Qy 421 CTATGTTCTCTTTTGTAGTGTGTATTAAGATGTCCTTTTGTAGCCACTCGAGAG 480
Db 4840 CTATGTTCTCTTTTGTAGTGTGTATTAAGATGTCCTTTTGTAGCCACTCGAGAG 4899
Qy 481 ATCTTACTTAACTCTAGTGGCAATGATTTGAGCTCTGAGTCAACGCAATGCTCTGT 540
Db 4900 ATCTTACTTAACTCTAGTGGCAATGATTTGAGCTCTGAGTCAACGCAATGCTCTGT 4959
Qy 541 AATCTACTGACCACTACTCTGAGTGTGTCTTAACTTAACTATTCACGCTGCT 600
Db 4960 AATCTACTGACCACTACTCTGAGTGTGTCTTAACTTAACTATTCACGCTGCT 5019
Qy 601 AGTAATTACCAATCATTTTACAACACTGTTCATGTGTAGGGCTGC 645
Db 5020 AGTAATTACCAATCATTTTACAACACTGTTCATGTGTAGGGCTGC 5064

RESULT 3

US-10-759-602-19
Sequence 19, Application US/10759602
Publication No. US20040143868A1
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
Belmar, Scott
Folkerts, Otto
Hopkins, Nicole
Menke, Michael A.
Paredy, Dayakar
Petolino, Joseph F.
Smith, Kelley
Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: DowAgrosciences LLC
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/10/759,602
; FILING DATE: 16-Jan-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kraus, Eric J
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 317 337 5110
;     TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 19:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 9335 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: circular
;   MOLECULE TYPE: DNA
;   SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-759-602-19

Query Match      100.0%; Score 645; DB 7; Length 9335;
Best Local Similarity 100.0%; Pred. No. 6,3e-164;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAGGTTCAATTCCTCTCTCTGTTATGTTCTTTATATTAATGCTCTGCAAAAGCT 60
DB 1758 GTCAGGTTCAATTCCTCTCTCTGTTATGTTCTTTATATTAATGCTCTGCAAAAGCT 1817
QY 61 ATTTAAAGCTTGATCTGAGTATATTAACAAGTTCACAAAGTTTGTACTTCAAG 120
DB 1818 ATTTAAAGCTTGATCTGAGTATATTAACAAGTTCACAAAGTTTGTACTTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAGTAATCCATATGAAGGTTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCAATTAAGATTATGAGTAATCCATATGAAGGTTGCAAG 1937
QY 181 AGAACAATGAAGGCAAAAGATTAACGAGATGAACCCATTACTAGCTTGGCTGTATCAGACC 240
DB 1938 AGAACAATGAAGGCAAAAGATTAACGAGATGAACCCATTACTAGCTTGGCTGTATCAGACC 1997
QY 241 AATTAATTTGAATGCACTTGTGTACATGCTTAAGTATTAAGAAAGTATGATGGAGAA 300
DB 1998 AATTAATTTGAATGCACTTGTGTACATGCTTAAGTATTAAGAAAGTATGATGGAGAA 2057
QY 301 ATCTATATTAATTTGGCTAACTCTTTAGTTACTTATTTGATGATGAGAAAGCTTACCAT 360
DB 2058 ATCTATATTAATTTGGCTAACTCTTTAGTTACTTATTTGATGATGAGAAAGCTTACCAT 2117
QY 361 GCCCATGCGAGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATGATTAATTACT 420
DB 2118 GCCCATGCGAGCCCTAATGTCCTGGGTGACATGATGAGCCAGTACTATGATTAATTACT 2177
QY 421 CTATGTTCTCTCTTTTGAAGTCTGTATTAAGATGCTTTTGAAGCACTCGAAG 480
DB 2178 CTATGTTCTCTCTTTTGAAGTCTGTATTAAGATGCTTTTGAAGCACTCGAAG 2237
QY 481 ATGTTTAACTTAACTAGTGGCAATGATGAGCTCTGAGTGCAAGCGATGCTCTGT 540
DB 2238 ATGTTTAACTTAACTAGTGGCAATGATGAGCTCTGAGTGCAAGCGATGCTCTGT 2297
QY 541 AATCTAAGTGTACCACTACTCTGTAGTGTGTGCTTAACTTAACTTAACTTAACTGAGCT 600
DB 2298 AATCTAAGTGTACCACTACTCTGTAGTGTGTGCTTAACTTAACTTAACTTAACTGAGCT 2357
QY 601 AGTAATTAACCAATCAATTTACACACATGTTTACATGTTAGGGCTGC 645
DB 2358 AGTAATTAACCAATCAATTTACACACATGTTTACATGTTAGGGCTGC 2402

RESULT 4
US-10-389-566-8
; Sequence 8; Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
```

```

; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Zea mays
US-10-389-566-8

Query Match      86.4%; Score 557; DB 7; Length 709;
Best Local Similarity 99.1%; Pred. No. 1.4e-140;
Matches 560; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 81 ATATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 140
DB 1 ACAATATTAACAAGTTAGTACACAAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGT 60
QY 141 GCATTAAGATTATGAGTAATCCATATGAAGTGTGTCAGAGAAATGAAGGCAAAAGAT 200
DB 61 GCATTAAGATTATGAGTAATCCATATGAAGTGTGTCAGAGAAATGAAGGCAAAAGAT 120
QY 201 AAACGATGAACCCATTACTAGCTTGGCTGTATCAGCAATTAATCTTGAATGCACTTG 260
DB 121 AAACGATGAACCCATTACTAGCTTGGCTGTATCAGCAATTAATCTTGAATGCACTTG 180
QY 261 TGCTAGCATGCTTAATATTAAGAAAGTATGAGATGGAGAAATCTATATTTTGGCTAA 320
DB 181 TGCTAGCATGCTTAATATTAAGAAAGTATGAGATGGAGAAATCTATATTTTGGCTAA 240
QY 321 CTTCCTTAAGTACTATGATGATGATGAGAAAGCTTACATTTGCCATGCGACCTTAATGT 380
DB 241 CTTCCTTAAGTACTATGATGATGATGAGAAAGCTTACATTTGCCATGCGACCTTAATGT 300
QY 381 CCGGTGACATGATGATGAGGCAAGTACTATGATTAATTAATCTATGTTCTCTTTTGA 440
DB 301 CCGGTGACATGATGATGAGGCAAGTACTATGATTAATTAATCTATGTTCTCTTTTGA 360
QY 441 GTGCTGTATTAAGATGCTCTTTTGAAGCACTCGAAGATGTTTACTTAACTTAACTAGT 500
DB 361 GTGCTGTATTAAGATGCTCTTTTGAAGCACTCGAAGATGTTTACTTAACTTAACTAGT 420
QY 501 CGCAATGATGAGGCTCTGAGTGCAACGATGCTCTGTATCTAAGTCTGACACTACT 560
DB 421 CGCAATGATGAGGCTCTGAGTGCAACGATGCTCTGTATCTAAGTCTGACACTACT 480
QY 561 CTGTAGTGTGTGTTTAACTCTTAATATTTCCAGTGTGCTATTAATCAATCAATTTAC 620
DB 481 CTGTAGTGTGTGTTTAACTCTTAATATTTCCAGTGTGCTATTAATCAATCAATTTAC 540
QY 621 AACACTGTTACATGTTAGGGCTGC 645
DB 541 AACACTGTTACATGTTAGGGCTGC 565

RESULT 5
US-10-389-566-217
; Sequence 217; Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
```

```

; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Zea mays
US-10-389-566-217

Query Match
Best Local Similarity 7.4%; Score 47.6; DB 7; Length 1119;
Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 584 AACTATTCACGCGGTAGTAATTAATCCATCATTTTCAACACGCTTACAGTGTAGGGCT 643
    |||
DB 15 AACAGGTAGCGACACAGTAATTAATCCATCATTTTACACACGCTGTACAGTGTAGGGCT 74
    |||
QY 644 GC 645
    ||
DB 75 GC 76

RESULT 6
US-10-367-094-117/c
; Sequence 117, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 117
; LENGTH: 138363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)..(138363)
; OTHER INFORMATION: n = A,T,C or G
US-10-367-094-117

Query Match
Best Local Similarity 6.8%; Score 43.8; DB 7; Length 138363;
Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATTGATGCTCTGACCAAGCTATAAGCTGATGACGATATATATTAACAAGTTA 96
    |||
DB 68785 TCTTGTACTGCTGTAGGAAGGCACTGACATTTATTAAGTGTGCTTACTATATTCATTA 68726
    |||
QY 97 GCTACACAAAGTTTGTACTCAAGCTCTTTTAACATATATATGTTGTGCAATAAGATTATAG 156
    |||
DB 68725 ACTTCATCAGTAAGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 68666
    |||
QY 157 TAATCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 211
    |||
DB 68665 TATATATATGCTGTGTTTTCMAAGCAAGTAATTAATTAATTAATTAATTAATTAATTA 68611
    |||

RESULT 7
US-10-741-600-17619/c
; Sequence 17619, Application US/10741600
; Publication No. US20050026169A1
```

```

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17619
; LENGTH: 130349
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17619

Query Match
Best Local Similarity 6.7%; Score 43.4; DB 8; Length 130349;
Matches 92; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATTGATGCTCTGACCAAGCTATAAGCTGATGACGATATATATTAACAAGTTA 96
    |||
DB 64786 TCTTGTACTGTGCTGTAGGAAGGACACTGACCATTTATTAAGTCTTACTATATCAATTA 64727
    |||
QY 97 GCTACAAAGTTTGTACTTCAAGTCTTTTAATATATGTTGGCAATTAAGATTATAG 156
    |||
DB 64726 ACTTCATCAKTAAGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 64667
    |||
QY 157 TAATCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 211
    |||
DB 64666 TATATATATGCTGTGTTTTCMAAGCAAGTAATTAATTAATTAATTAATTAATTAATTA 64612
    |||

RESULT 8
US-10-706-635-23/c
; Sequence 23, Application US/10706635
; Publication No. US20050014263A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Richard W.
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
; TITLE OF INVENTION: Vertebrate Cells
; FILE REFERENCE: UF-221CX21
; CURRENT APPLICATION NUMBER: US/10/706,635
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/086,651
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 09/662,254
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/224,479
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 50000
; TYPE: DNA
; ORGANISM: Ambacta moorei entomopoxvirus
US-10-706-635-23

Query Match
Best Local Similarity 6.6%; Score 42.8; DB 8; Length 50000;
Matches 146; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 27 TTATGTTCTTATATATACATGCTCTGACAAAGCTATTAAGCTGATGACGATATATTA 86
    |||
DB 11134 TGATATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11075
    |||
QY 87 TAAACAAGTATGCTACCAAGTTTGTACTTCAAGTCTTTTAATATATGTTGGTGCAATA 146
    |||
DB 11074 TAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 11015
    |||
QY 147 AGATTATGATATCATATGAAGGTGTGCAAGACATGAAGCAAGCAAGCAAGCAAGCAAGCA 206
    |||
DB 11014 TTATTAATCGCATGTTTGCAACACAGATTGAAAAAATTAATTAATTAATTAATTAATTA 10955
    |||
```


/ PRIOR FILING DATE: 2001-07-02
/ PRIOR APPLICATION NUMBER: DE 10032529.7
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: DE 10043826.1
/ PRIOR FILING DATE: 2000-09-01
/ NUMBER OF SEQ ID NOS: 2424
/ SEQ ID NO 2123
/ LENGTH: 5376
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically created genomic DNA (Homo sapiens)
US-10-311-455-2123

Query Match 6.1%; Score 39.4; DB 6; Length 5376;
Best Local Similarity 47.4%; Pred. No. 13;
Matches 118; Conservative 0; Mismatches 131; Indels 0; Gaps 0;
QY 4 AAGGTCGAATTCGCTCTGCTGTTAGTCTTTATATTACATGCTGACAAAGCTATA 63
DB 1188 AAAATTGAATTTGGATTTTATTATTTATATATATAAATTAAATTAAAGATGATTAA 1247
QY 64 AAGCTTGATACGTCAGTATATATTAACAAGTTAGCTACACAGTTTGTACTTCAAGTCT 123
DB 1248 AGATTTAAATGTAAATTTTAAATTTAATAAATTTTAGAAGTAAATTTAGTAAATTAAT 1307
QY 124 TTTACTATATGTGTGTGCAATAGATTAAGATTAATCCATATGAAGGTGTGCAAGAGA 183
DB 1308 TTGAATATATAGTAGAGTAAGATTTTGAAGAAGATGTAAAGTAATGTGATAAA 1367
QY 184 ACATGAAGGCAAAAGATTAACGATGAACCATTAAGCTTGGCTGATCAGACCAAT 243
DB 1368 AGAAAAAATTAAATTAATGATATTAAATTAATTAAGAGTTTGTATTAGTAATTAAT 1427
QY 244 AACTTGAAA 252
DB 1428 TATTATATA 1436

Search completed: February 12, 2006, 00:19:58
Job time : 831 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:58:37 ; Search time 179 Seconds
(without alignments)
6405.180 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645

Sequence: 1 GTCAAGTTCATCTGCTT.....TGTTCATGTGTAGGGCTGC 645

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1.COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5.COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 7: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 8: /cgn2_6/prodata/1/ina/6.COMB.seq:*
- 9: /cgn2_6/prodata/1/ina/6.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	100.0	6550	3	US-09-097-319A-1
2	645	100.0	6550	3	US-09-643-971-1
3	645	100.0	9335	3	US-09-097-319A-19
4	645	100.0	9335	3	US-09-643-971-19
5	43.8	6.8	83178	3	US-09-949-016-14606
6	43.4	6.7	601	3	US-09-949-016-103411
7	42.8	6.6	50000	3	US-09-662-2548-23
8	40.8	6.3	1055	3	US-09-806-7088-23
9	40.2	6.2	1141	3	US-09-806-7088-22
10	39.6	6.1	124480	3	US-09-949-016-15921
11	38.2	5.9	7218	2	US-08-232-463-14
12	37.8	5.9	601	3	US-09-949-016-178415
13	37.8	5.9	99830	3	US-09-949-016-16859
14	37.6	5.8	601	3	US-09-949-016-163480
15	37.6	5.8	50000	3	US-09-662-2548-25
16	37.6	5.8	94593	3	US-09-949-016-16324
17	37.6	5.8	580073	3	US-08-545-528D-1
18	37.4	5.8	601	3	US-09-949-016-178416
19	37.2	5.8	601	3	US-09-949-016-163479
20	37.2	5.8	1844	3	US-09-123-912-88
21	37.2	5.8	1844	3	US-09-643-597-88
22	37.2	5.8	1844	3	US-09-480-884A-88
23	37.2	5.8	1844	3	US-09-542-615A-88
24	37.2	5.8	1844	3	US-09-606-421B-88

25	37.2	5.8	1844	3	US-09-221-107-88	Sequence 88, Appl
26	37.2	5.8	1844	3	US-09-466-396A-88	Sequence 88, Appl
27	37.2	5.8	1844	3	US-09-476-496A-88	Sequence 88, Appl
28	37.2	5.8	1844	3	US-09-630-940B-88	Sequence 88, Appl
29	37.2	5.8	1844	3	US-09-285-479-88	Sequence 88, Appl
30	37.2	5.8	1844	3	US-10-007-700-88	Sequence 14100, A
31	37.2	5.8	32721	3	US-09-949-016-14100	Sequence 14100, A
32	37	5.7	832	3	US-09-621-976-2813	Sequence 2813, Ap
33	36.8	5.7	48119	3	US-09-949-016-12003	Sequence 12003, A
34	36.8	5.7	48119	3	US-09-949-016-13177	Sequence 13177, A
35	36.8	5.7	50000	3	US-09-662-2548-26	Sequence 26, Appl
36	36.8	5.7	786431	3	US-09-751-389-3	Sequence 3, Appl
37	36.6	5.7	573	3	US-09-248-796A-6562	Sequence 6562, Ap
38	36.6	5.7	601	3	US-09-949-016-15527	Sequence 15527, A
39	36.4	5.6	38206	3	US-09-949-016-15527	Sequence 15527, A
40	36.4	5.6	124480	3	US-09-949-016-15921	Sequence 15921, A
41	36	5.6	1141	3	US-09-806-7088-22	Sequence 22, Appl
42	36	5.6	5619	3	US-09-799-451-241	Sequence 241, App
43	35.6	5.5	693	3	US-09-248-796A-1677	Sequence 1677, Ap
44	35.4	5.5	1818	3	US-09-107-532A-2423	Sequence 2423, Ap
45	35.4	5.5	232547	3	US-09-949-016-16603	Sequence 16603, A

ALIGNMENTS

RESULT 1
US-09-097-319A-1
; Sequence 1, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Attnley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Daykar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dowlati, Patent Department
; STREET: 9330 Zionville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6550 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: exon

```
/ LOCATION: 4201..4425
/ OTHER INFORMATION: /product= "Peroxidase"
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 4426..5058
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5059..5250
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 5251..5382
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5383..5548
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: 5549..5649
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: 5650..6065
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649
/ LOCATION: ..6068)
/ US-09-097-319A-1
```

Query Match 100.0%; Score 645; DB 3; Length 6550;

Best Local Similarity 100.0%; Pred. No. 9.9e-170; Indels 0; Gaps 0;

Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GTCAGGTTCAATTCCTCTCTCTGTTATGTTCTTTATATTAATGCTCTGCAAAAGCT 60
DB 4420 GTCAGGTTCAATTCCTCTCTCTGTTATGTTCTTTATATTAATGCTCTGCAAAAGCT 4479
QY 61 ATAAAGCTTGATCTGAGTATATATATTAACAAGTTACTACACAAAGTTTGACTTAAAG 120
DB 4480 ATAAAGCTTGATCTGAGTATATATATTAACAAGTTACTACACAAAGTTTGACTTAAAG 4539
QY 121 TCTTTTAACTATATGTTGGTGAATAAGATTATGAGTAATCCATATAGAAGTGTGCAAG 180
DB 4540 TCTTTTAACTATATGTTGGTGAATAAGATTATGAGTAATCCATATAGAAGTGTGCAAG 4599
QY 181 AGAATCATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGACC 240
DB 4600 AGAATCATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTTGGCTGTACAGACC 4659
QY 241 AATTAAGTTGAATGCACTTGTGCTAGCATGCTTAAGTATTGAAAAAGTACATGGAGAG 300
DB 4660 AATTAAGTTGAATGCACTTGTGCTAGCATGCTTAAGTATTGAAAAAGTACATGGAGAG 4719
QY 301 ATCTATATTTATTTTGGGTAACCTTCTTAAGTACTATTAATGATGATGAGAAAGCTTACAT 360
DB 4720 ATCTATATTTATTTTGGGTAACCTTCTTAAGTACTATTAATGATGATGAGAAAGCTTACAT 4779
QY 361 GCCCATCCAGCCCTTAATGTCCTCGGTGACATGATTTGAGCCAGTACTATTAATTTTACT 420
DB 4780 GCCCATCCAGCCCTTAATGTCCTCGGTGACATGATTTGAGCCAGTACTATTAATTTTACT 4839
QY 421 CTATTTGTTCTCTTTTGAAGTCTGTATTAAGATGTCCTTTTGAAGCCACTGGAAGAG 480
DB 4840 CTATTTGTTCTCTTTTGAAGTCTGTATTAAGATGTCCTTTTGAAGCCACTGGAAGAG 4899
QY 481 ATGTTTACTTAACCTCTAGTGGCAATGTTGGAAGCTGTCAGTGAAGCATGAGCTCTGCT 540
DB 4900 ATGTTTACTTAACCTCTAGTGGCAATGTTGGAAGCTGTCAGTGAAGCATGAGCTCTGCT 4959
QY 541 AATCTAGTGCACCACTACTCTGTAGTGTGCTTAAACTTAACTTAATTCACAGTGGCT 600
DB 4960 AATCTAGTGCACCACTACTCTGTAGTGTGCTTAAACTTAACTTAATTCACAGTGGCT 5019
QY 601 AGTAATTAACCAATCAATTTTAAACAAGCTGTTACATGTGTAGGGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTTTAAACAAGCTGTTACATGTGTAGGGGCTGC 5064
```

RESULT 2

US-09-643-971-1

/ Sequence 1, Application US/09643971

/ Patent No. 6699984

/ GENERAL INFORMATION:

/ APPLICANT: Ainley, Michael

/ APPLICANT: Armstrong, Katherine

/ APPLICANT: Belmar, Scott

/ APPLICANT: Folkerts, Otto

/ APPLICANT: Hopkins, Nicole

/ APPLICANT: Menke, Michael A.

/ APPLICANT: Paredy, Dayakar

/ APPLICANT: Petolino, Joseph F.

/ APPLICANT: Smith, Kelley

/ APPLICANT: Woosley, Aaron

/ TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

/ NUMBER OF SEQUENCES: 59

/ CORRESPONDENCE ADDRESSES:

/ ADDRESSER: Dowelanco Patent Department

/ STREET: 9330 Zionville Road

/ CITY: Indianapolis

/ STATE: Indiana

/ COUNTRY: USA

/ ZIP: 46268

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/643,971

/ FILING DATE:

/ CLASSIFICATION:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Stuart, Donald R

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 317 337 4816

/ TELEFAX: 317 337 4847

/ INFORMATION FOR SEQ. ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 6550 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 4201..4425

/ OTHER INFORMATION: /product= "Peroxidase"

/ FEATURE:

/ NAME/KEY: intron

/ LOCATION: 4426..5058

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 5059..5250

/ FEATURE:

/ NAME/KEY: intron

/ LOCATION: 5251..5382

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 5383..5548

/ FEATURE:

/ NAME/KEY: intron

/ LOCATION: 5549..5649

/ FEATURE:

/ NAME/KEY: exon

/ LOCATION: 5650..6065

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649

/ LOCATION: ..6068)

US-09-643-971-1

Query Match 100.0%; Score 645; DB 3; Length 6550;
Best Local Similarity 100.0%; Pred. No. 9.9e-170;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAAGTTCATATTCGCTCTCTGTATGTTCTTTATATTAATGACAGCTGCAAAAGCT 60
|||||
4420 GTCAAGTTCATATTCGCTCTCTGTATGTTCTTTATATTAATGACAGCTGCAAAAGCT 4479
61 ATAAAGCTTGATATCTGAGATATATATTAACAAGTATGCTACACAGTTTGTACTTCAAG 120
4480 ATAAAGCTTGATATCTGAGATATATATTAACAAGTATGCTACACAGTTTGTACTTCAAG 4539
121 TCTTTAATCTATATGTTGGTGAATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 180
4540 TCTTTAATCTATATGTTGGTGAATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 4599
181 AGAATGAAAGGCAAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 240
4600 AGAATGAAAGGCAAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 4659
241 AATTAATGAAATGCACTTGCTGATGATGCTTAAGATTAAGATTAAGATTAAGATTAAGATTA 300
4660 AATTAATGAAATGCACTTGCTGATGATGCTTAAGATTAAGATTAAGATTAAGATTAAGATTA 4719
301 ATCTATATTAATTTTGGCTAATCTTCTTATGTTACTATGATTAAGATTAAGATTAAGATTA 360
4720 ATCTATATTAATTTTGGCTAATCTTCTTATGTTACTATGATTAAGATTAAGATTAAGATTA 4779
361 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
4780 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4839
421 CTATGTTCTCTTTTGAAGTCTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 480
4840 CTATGTTCTCTTTTGAAGTCTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 4899
481 ATGTTTAACTTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
4900 ATGTTTAACTTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4959
541 AATCTACTGTCACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
4960 AATCTACTGTCACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5019
601 AGTAATTAACCAATCAATTAACAACCTGTTACATGTTAGGGCTGC 645
5020 AGTAATTAACCAATCAATTAACAACCTGTTACATGTTAGGGCTGC 5064

RESULT 3

US-09-097-319A-19
Sequence 19, Application US/09097319A
Patent No. 6384207

GENERAL INFORMATION:

APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelance Patent Department
STREET: 9330 Zionville Road
CITY: Indianapolis
STATE: Indiana

COUNTRY: USA

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,319A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Stuart, Donald R

TELEPHONE: 317 337 4816

TELEFAX: 317 337 4816

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 935 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA

US-09-097-319A-19

Query Match 100.0%; Score 645; DB 3; Length 9335;
Best Local Similarity 100.0%; Pred. No. 1.1e-169;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCAAGTTCATATTCGCTCTCTGTATGTTCTTTATATTAATGACAGCTGCAAAAGCT 60
|||||
1758 GTCAAGTTCATATTCGCTCTCTGTATGTTCTTTATATTAATGACAGCTGCAAAAGCT 1817
61 ATAAAGCTTGATATCTGAGATATATATTAACAAGTATGCTACACAGTTTGTACTTCAAG 120
1818 ATAAAGCTTGATATCTGAGATATATATTAACAAGTATGCTACACAGTTTGTACTTCAAG 1877
121 TCTTTAATCTATATGTTGGTGAATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 180
1878 TCTTTAATCTATATGTTGGTGAATAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1937
181 AGAATGAAAGGCAAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 240
1938 AGAATGAAAGGCAAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1997
241 AATTAATGAAATGCACTTGCTGATGATGCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 300
1998 AATTAATGAAATGCACTTGCTGATGATGCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2057
301 ATCTATATTAATTTTGGCTAATCTTCTTATGTTACTATGATTAAGATTAAGATTAAGATTAAGATTA 360
2058 ATCTATATTAATTTTGGCTAATCTTCTTATGTTACTATGATTAAGATTAAGATTAAGATTAAGATTA 2117
361 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
2118 GCCCATGCGAGCCCTAATGTCGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2177
421 CTATGTTCTCTTTTGAAGTCTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 480
2178 CTATGTTCTCTTTTGAAGTCTGTATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 2237
481 ATGTTTAACTTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
2238 ATGTTTAACTTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2297
541 AATCTACTGTCACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
2298 AATCTACTGTCACCACTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2357
601 AGTAATTAACCAATCAATTAACAACCTGTTACATGTTAGGGCTGC 645
2358 AGTAATTAACCAATCAATTAACAACCTGTTACATGTTAGGGCTGC 2402

```
RESULT 4
US-09-643-971-19
; Sequence 19, Application US/09643971
; Patent No. 6699984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowdanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4846
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-09-643-971-19

Query Match 100.0%; Score 645; DB 3; Length 935;
Best Local Similarity 100.0%; Pred. No. 1.1e-169;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAAGTTCATTCTGCTCTGCTTGTATTGTTTATATTAATGCTGACAAAGCT 60
DB 1758 GTCAAGTTCATTCTGCTCTGCTTGTATTGTTTATATTAATGCTGACAAAGCT 1817
QY 61 ATAAAGTTGATCGAGTATATTAATTAACAAGTTAGTACACAAGTTTGTACTTCAAG 120
DB 1818 ATAAAGTTGATCGAGTATATTAATTAACAAGTTAGTACACAAGTTTGTACTTCAAG 1877
QY 121 TCTTTTAATAATATGTTGGTGAATTAAGATTATGATTAATCATATGAAGGTGGCAAG 180
DB 1878 TCTTTTAATAATATGTTGGTGAATTAAGATTATGATTAATCATATGAAGGTGGCAAG 1937
QY 181 AGAACAATGAAGGCAAGATTAACGATGAACCCATTACTGCTTTGGCTGTATCAACC 240
DB 1938 AGAACAATGAAGGCAAGATTAACGATGAACCCATTACTGCTTTGGCTGTATCAACC 1997
QY 241 AATACTTGAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGGATGATGGAGA 300
DB 1998 AATACTTGAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGGATGATGGAGA 2057
QY 301 ATCTATATATATTTGGCTAACTCTTTAGTTACTATTAATGATTAAGAAAGCCTTACATT 360
```

```
DB 2058 ATCTATATATATTTGGCTAACTCTTTAGTTACTATTAATGATTAAGAAAGCCTTACATT 2117
QY 361 GCCCATGCGAGCCCTAATATGCCGGGACATGATTTAGCCAGACTATGATTAATTACT 420
DB 2118 GCCCATGCGAGCCCTAATATGCCGGGACATGATTTAGCCAGACTATGATTAATTACT 2177
QY 421 CTATGTTCTCTTTTGTGAGTGTGATTAAGATGTCCTTTTGTGAGCCACTCGAAG 480
DB 2178 CTATGTTCTCTTTTGTGAGTGTGATTAAGATGTCCTTTTGTGAGCCACTCGAAG 2237
QY 481 ATGTTTACTTAACTCTAAGCGCAATGATTTGAGAGCTCTAGTGCAACGATGTGCTGT 540
DB 2238 ATGTTTACTTAACTCTAAGCGCAATGATTTGAGAGCTCTAGTGCAACGATGTGCTGT 2297
QY 541 AATCTACTGTCACCACTACTGTTAGTGTGCTTAACTCTAATCTATTCAGAGGCT 600
DB 2298 AATCTACTGTCACCACTACTGTTAGTGTGCTTAACTCTAATCTATTCAGAGGCT 2257
QY 601 AGTAATTACCAATCATTTTCAACACTGTATACATGTAGGGCTGC 645
DB 2358 AGTAATTACCAATCATTTTCAACACTGTATACATGTAGGGCTGC 2402
```

```
RESULT 5
US-09-949-016-14606/c
; Sequence 14606, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14606
; LENGTH: 83178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14606

Query Match 6.8%; Score 43.8; DB 3; Length 83178;
Best Local Similarity 53.1%; Pred. No. 0.091;
Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
```

```
QY 37 TATATTACATGCTCTGCAACAAGCTATTAAGCTGATACGATATATTAACAAGTTA 96
DB 60785 TCTTTGACTTGCCTGTGGAAGGCACTGACATTTATTTAATCTCTAATCAATTA 60726
QY 97 GTACACAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGGCAATAAGATTATGAG 156
DB 60725 ACTTCATCACTAAGTACTAATAAATCTTTGATGATACCTTAACAAATTTCTGTATG 60666
QY 157 TAAATCATGAAGGTTGTCAGAGAAACAATGAAGGCAAGTAACGATGA 211
DB 60665 TATTAATATATGCTTGTGTTTCAACGAAGATTAATGTCATTGTTAAACAGTTCA 60611
```

```
RESULT 6
US-09-949-016-103411/c
; Sequence 103411, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CU001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 103411
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-103411

Query Match 6.7%; Score 43.4; DB 3; Length 601;
Best Local Similarity 52.6%; Pred. No. 0.022;
Matches 92; Conservative 1; Mismatches 82; Indels 0; Gaps 0;

QY 37 TATATACAGCTCTGCAAGCTATTAAGCTGATCTGAGTATTAATTAACAAGTTA 96
DB 370 TCTGTACTGCTGTAGGAGGACCTGACATTTATTACTGCTTACTATTCATATA 311
QY 97 GCTACACAGTTTGTACTTCAAGTCTTTAATCTATATGTTGGTCAATGAATATGAG 156
DB 310 ACTTCATCATTAAGTACTGAAATATCTTGATGATCCCTTAACAAATTTCTGTATGG 251
QY 157 TAATCATATGAGTGTGTCAGAGAACATGAAGCAAGATTAACGATGA 211
DB 250 TATATATATGCTGTGTTTCAACAGAAATTAATGCAATGTTTAAAGTTCA 196

RESULT 7
US-09-662-254B-23/c
/ Sequence 23, Application US/09662254B
/ Patent No. 6931145
/ GENERAL INFORMATION:
/ APPLICANT: Moyer, Richard W.
/ APPLICANT: LI, YI
/ TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
/ TITLE OF INVENTION: Vertebrate Cells
/ FILE REFERENCE: UF-221C1X1
/ CURRENT APPLICATION NUMBER: US/09/662,254B
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 09/086,651
/ PRIOR FILING DATE: 1998-05-29
/ PRIOR APPLICATION NUMBER: 60/224,479
/ PRIOR FILING DATE: 2000-08-10
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 23
/ LENGTH: 50000
/ TYPE: DNA
/ ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-23

Query Match 6.6%; Score 42.8; DB 3; Length 50000;
Best Local Similarity 45.9%; Pred. No. 0.15;
Matches 166; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
QY 27 TTAGTCTTTATATTAATGCTCTGCAAGCTATTAAGCTGATCTGAGTATTAATTA 86
DB 11134 TGAATATAATGTAATATTAATGATATTTCTATTAAGTATTAATTAATTAATTA 11075
QY 87 TAAACAGTATGACACAGCTTTGATCTTCAAGTCTTTAATCTATATGTTGGTGAAT 146
DB 11074 TAAATATATAAAGAAAGCAATTTTATCTGTAATATTTTAAATTTTAAAGTATATC 11015
QY 147 AGATATGATATCATATGAGTGTGCAAGAGAACATGAAGCAAGATTAACG 206

DB 11014 TTAATTCGCAAGTTTGCAACAGAGTTGAAAAAATCAAAATTAATTAATTAAT 10955
QY 207 ATGAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 266
DB 10954 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 10895
QY 267 CATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 326
DB 10894 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10835
QY 327 TAGTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 344
DB 10834 AAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 10817

RESULT 8
US-09-806-708B-23
/ Sequence 23, Application US/09806708B
/ Patent No. 6784342
/ GENERAL INFORMATION:
/ APPLICANT: The University of British Columbia
/ TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
/ FILE REFERENCE: 4810-58741
/ CURRENT APPLICATION NUMBER: US/09/806,708B
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: US 60/147,133
/ PRIOR FILING DATE: 1999-08-04
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: Patent version 3.0
/ SEQ ID NO 23
/ LENGTH: 1055
/ TYPE: DNA
/ ORGANISM: Artificial sequence
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (1)-(1055)
/ OTHER INFORMATION: consensus sequence of A.T. and L.A. FAE1 promoters
US-09-806-708B-23

Query Match 6.3%; Score 40.8; DB 3; Length 1055;
Best Local Similarity 19.8%; Pred. No. 0.14;
Matches 90; Conservative 120; Mismatches 244; Indels 0; Gaps 0;

QY 58 GCTATAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 117
DB 45 RCYARRWMTTAYVMTATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 104
QY 118 AAGCTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 177
DB 105 WRTGTWMTKTNNAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 164
QY 178 AAGAGAACATGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 237
DB 165 NSTRTTYYTWKMKCKKSAARARTRBARRMYTAMARCTGATAMAAATYMN 224
QY 238 ACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 297
DB 225 NNNNAKAKKRAATGWRKSNCTCTAGTTTBRATCCAAATCGAGMATKKTWTS 284
QY 298 AGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 357
DB 285 AAGMTNNNNNNNNNTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 344
QY 358 ATGGCCATGACGACCTTAATGATGATGATGATGATGATGATGATGATGATGATGAT 417
DB 345 GTTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 404
QY 418 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 477
DB 405 TCTMNTTAAKATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 464
QY 478 AAGATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 511

Db 465 ACTWTTYKRCCTAANTAAWYTKSSANCTSRTR 498

```

RESULT 9
US-09-806-708B-22/c
: Sequence 22. Application US/09806708B
: Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent version 3.0
SEQ ID NO 22
:
: LENGTH: 1141
: TYPE: DNA
: ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(1141)
:
: OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

```

Query Match 6.2%; Score 40.2; DB 3; Length 1141;
Best Local Similarity 10.0%; Pred. No. 0.21;
Matches 63; Conservative 245; Mismatches 323; Indels 1; Gaps 1;

Qy	10	CAATTCGCTCTCGTATGTTCTTTATATCAATGCTGCAAGACGTAATTAAGCTT	69
Db	770	HAAVTTTHIDMCKYKMTWYDMTMTTBTTHTRKNTSTNTNNNNNNMACTNNNNNN	711
Qy	70	GATACGTGACGATATATAACAAGTTAGTACACAAGTTTGATCTCAAGCTCTTTTAA	129
Db	710	MMKAYYAAATNNMGCMNNNTDARTNNTTMMRRMWTMTKTFWYSTTRHHYATATNNN	651
Qy	130	TATATGTGGTGCAATTAAGATTATAGATAATCATATGAAGGTGTGGAAGAAACATGA	181
Db	650	NNNNNNNNNNNSCCTTRMTWTRMTKMDGATVRKRYKMRPTCTTYVDVADSWMYTA	591
Qy	190	AAGCAAGATTAACGATGAACCCATTACTAGCTTGGCTGTATCAGACCAATACCTTG	249
Db	590	MMRRCRVYTRNNYCKSYAHSYWNSSNNMYRYSABNNSSAARTTNNMMGBV	531
Qy	250	AAATGCACTTGCTAGCATGCTTAAGATTAGAAAAAGTAGACGAGAACTATATT	309
Db	530	RMBAGMMTRHNNNNNTDTRYYWVV-KEMABTTTVDVSMCAKSMRGNNMMAKMW	472
Qy	310	ATTTGGCTAACTCTTTAGTTACTATGATTTGAGAGAAAGCCATCACTGGCCATGCC	36
Db	471	AAANDACAMDHMYTMMGNNTMMRRMAYKMMNNAMCRAYCCNNNNRACVNHKHKMRWT	412
Qy	370	AGCCCTAATGCTCCCGTGACATGATTGAGCCAGTACTAATTAATTTCTATTGTC	428
Db	411	WKYMKRAACNNNBKAMRYRVAWMYSRJOTJTDMMWTSDBBHWITVDTYMMRANNN	35
Qy	430	TCCTTTTGAAGTGTATAGATGTCCTTTTTTGAAGCACTGGAAGAAGTTTACT	488
Db	351	NNNNMBCKTSSMMWMDHNTHTCTGANNYTGSAVBMAMSSAAGANBVTYVMCWRMT	292
Qy	490	TAACTCAAGGCCAATGATTGGAGTCTCAGGCAAGCAAGTGCCTGTAACTCTAG	548
Db	291	YMGKTMNNNNNNKAMTYRTKYAKCNRYYDTATVBTBKRYKCYAVYBVTBNTGKA	23
Qy	550	TCAACCACTCTGTAGTGTGCTTAAACTTAATCTAATTCACATGCGTAGTAATTAAC	608
Db	231	HMBWMMRABRHSNNMMVVKCRNKKYVSWYHAYRBYKMBAYGANNKKDYMANNHMCAT	172
Qy	610	CAATCATTTACAACCTGTTACATGCTGTAGGG	641

```

      ::::|::::: : | | ::::
Db 171 NNNMMWWYAYMHMHKKGAWTNNKTABRD 140

```

```

RESULT 10
US-09-949-016-15921/c
: Sequence 15921, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15921
: LENGTH: 124480
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-15921

```

Query Match	6.1%;	Score 39.6;	DB 3;	Length 124480;
Best Local Similarity	51.7%;	Pred. 1.5;		
Matches	90;	Conservative	0;	Mismatches 84;
				Indels 0;
				Gaps 0;

QY	237	GACCAATTAACCTTAAAAATGCACCTTGTCAGACAGCCCAAGATATTAAGAAAGATGACATGG	296
QY	37447	GACTTAAAAACAGAGAGAGAACTTTTATCTTAAAGCTTGTGAAATGGAATGTAGCAAGAG	37388
QY	297	GAGATCTATATTAATTTTGGCTAACTCTTTAGTTACTATATGATAGAAAGCTAC	356
Db	37387	CAGATTTTANATGGTTTTTGGCTTCTTTNATCCTTTCTTTCAAGGTAAACAATCTATC	37328
QY	357	CATTGCCCAAGCCAGCCCTTATATGCTCCCGGTACATATGAGCCAGTACTATAGA	410
Db	37327	TTTAGAGATTGTATTAACAATAGCCCTTCCCTTCAGAAACATACACTTCTATGA	37274

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

```
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpct-F16
US-08-232-463-14
```

```
Query Match 5.9%; Score 38.2; DB 2; Length 7218;
Best Local Similarity 6.5%; Pred. No. 1.4;
Matches 22; Conservative 17; Mismatches 144; Indels 0; Gaps 0;
```

```
QY 302 TCATATATTATTTGGCTACTCTTCTTATGTTACTATTGATGAGAAAGCTAACCTTGG 361
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1142 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1201
QY 362 CCCAGGCAGCCGTAATGCCGGTGACATGATGAGCCAGTCTATGATTAATTACTG 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1202 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1261
QY 422 TATGTCTCTCTTTTGTAGTGTCTTAAGATGTCCTTTTGTAGCCACTGAGAGA 481
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1262 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1321
QY 482 TGTCTACTTACTCTAGTGGCAATGATGAGCTCTCACTGCAAGCAGTGTCTGTA 541
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1322 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1381
QY 542 ATCTACGTGACACACTGCTAGTGTGCTTAACCTAATCATCTACAGTGTGCTA 601
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1382 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1441
QY 602 GTAATTACCAATCATTTACCAACTGTTACATGTGTA 638
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1442 ATCTCTATCTCTTTTACTACTTGTGATGATAGTGA 1478
```

```
RESULT 12
US-09-949-016-178415/c
; Sequence 178415, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaSeq for Windows Version 4.0
; SEQ ID NO 178415
; LENGTH: 601
; TYPE: DNA
```

```
ORGANISM: Human
US-09-949-016-178415
```

```
Query Match 5.9%; Score 37.8; DB 3; Length 601;
Best Local Similarity 50.8%; Pred. No. 0.81;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
```

```
QY 134 TGTGTGCAATTAAGTATTAGTATCCATATGAGAGTGTCCAGAGAACTGAAGG 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 TGTACTGAGTCAGAAATCAGGATTTAGTCTAGGGTTTGCAACAAGAGATTAAGG 467
QY 194 CAAAGATTAACGAGTAAACCATTAAGCTTTGCTGTATCAGACCAATTAAGTGAAT 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 ACAAAATTTATTTGAAATCAGTTACTACTACAGCATCTATATCTTAACCTTACTG 407
QY 254 GCACTGTGTCTAGATGCTTAAGTATTGAAAAGTGAAGCATGGAGAAATCTATATTA 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 406 GGCTATTGTATCAATTCACACAGCATACCAAAACATGGAAGATTCAATGTATCTTA 350
```

RESULT 13

```
US-09-949-016-16859/c
; Sequence 16859, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
```

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```
; FILE REFERENCE: C1001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
```

```
; PRIOR FILING DATE: 2000-04-14
```

```
; PRIOR APPLICATION NUMBER: 60/241,755
```

```
; PRIOR FILING DATE: 2000-10-20
```

```
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
```

```
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
```

```
; NUMBER OF SEQ ID NOS: 207012
```

```
; SOFTWARE: FaSeq for Windows Version 4.0
```

```
; SEQ ID NO 16859
```

```
; LENGTH: 99830
```

```
; TYPE: DNA
```

```
; ORGANISM: Human
```

```
; FEATURE: misc_feature
```

```
; NAME/KEY: (1)...(99830)
```

```
; LOCATION: (1)...(99830)
```

```
; OTHER INFORMATION: n = A,T,C or G
```

```
US-09-949-016-16859
```

```
Query Match 5.9%; Score 37.8; DB 3; Length 99830;
Best Local Similarity 50.8%; Pred. No. 4.5;
Matches 90; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
```

```
QY 134 TGTGTGCAATTAAGTATTAGTATCCATATGAGAGTGTCCAGAGAACTGAAGG 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 7667 TGTACTGAGTCAGAAATCAGGATTTAGTCTAGGGTTTGCAACAAGAGATTAAGG 7608
QY 194 CAAAGATTAACGAGTAAACCATTAAGCTTTGCTGTATCAGACCAATTAAGTGAAT 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 7607 ACAAAATTTATTTGAAATCAGTTACTACTACAGCATCTATATCTTAACCTTACTG 7548
QY 254 GCACTGTGTCTAGATGCTTAAGTATTGAAAAGTGAAGCATGGAGAAATCTATATTA 310
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 7547 GGCTATTGTATCAATTCACACAGCATACCAAAACATGGAAGATTCAATGTATCTTA 7491
```

RESULT 14

```
US-09-949-016-163480/c
; Sequence 163480, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
```

```
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

```

1  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
2  FILE REFERENCE: CLO01107
3  CURRENT APPLICATION NUMBER: US/09/949,016
4  CURRENT FILING DATE: 2000-04-14
5  PRIOR APPLICATION NUMBER: 60/241,755
6  PRIOR FILING DATE: 2000-10-20
7  PRIOR APPLICATION NUMBER: 60/237,768
8  PRIOR FILING DATE: 2000-10-03
9  PRIOR APPLICATION NUMBER: 60/231,498
10 PRIOR FILING DATE: 2000-09-08
11 NUMBER OF SEQ ID NOS: 207012
12 SOFTWARE: FASTSEQ for Windows Version 4.0
13 SEQ ID NO: 163480
14 LENGTH: 601
15 TYPE: DNA
16 ORGANISM: Human
17 US-09-949-016-163480

```

Query Match	5.8%	Score 37.6;	DB 3;	Length 601;
Best Local Similarity	49.5%;	Pred. No. 0.92;		
Matches 97;	Conservative	0;	Mismatches 99;	Indels 0;
			Gaps	0;

Oy	33	CTTTATATATACATCTCGACAAAGCTATAAAGCTGATCTGAGATATATATATACAA	92
Db	240	TTTTTTGGTTCCTTTCTGAGTAGATATTTGCATGCTAACAAAGTATTTTCATTTAAATTA	181
Oy	93	GTTAGCTACACAAGTTTGTGATCTCAAGCTCTTTAATACTATATGTTGGTCAATAAGATT	152
Db	180	ATATTTTAGTATAGTTTGGTTTTTTTAAAGGTTTTCTTTAGATTGTTTAAACAAATTTTA	121
Oy	153	TGAGTATATCATATGATAGGTGTTGCAGAGAAATGAAAGCAAAATTAACGATGAC	212
Db	120	ATTTTAAACATTCGTAATATGTTAAACACAGATCAATAGGAGAAATGATTTGGGGTTT	61
Oy	213	CCATTACTAGCTTTGG	228
Db	60	CATTTTAAAGATTAG	45

```

RESULT 15
US-09-662-254B-25/c
: Sequence 25, Application US/09662254B
: Patent No. 6933145
: GENERAL INFORMATION:
: APPLICANT: Moyer, Richard W.
: APPLICANT: Li, Yi
: APPLICANT: Bawden, Alison Louise
: TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologous
: TITLE OF INVENTION: Vertebrate Cells
: FILE REFERENCE: US-221C1X1
: CURRENT APPLICATION NUMBER: US/09/662,254B
: CURRENT FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: 09/086,651
: PRIOR FILING DATE: 1998-05-29
: PRIOR APPLICATION NUMBER: 60/224,479
: PRIOR FILING DATE: 2000-08-10
: NUMBER OF SEQ ID NOS: 80
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 25
: LENGTH: 50000
: TYPE: DNA
: ORGANISM: Ambacta moorei entomopoxvirus
US-09-662-254B-25

```

Query Match	5.8%	Score 37.6;	DB 3;	Length 50000;
Best Local Similarity	45.8%	Pred. No. 4.1;		
Matches 130; Conservative	0;	Mismatches 154;	Indels 0;	Gaps 0;

[illegible]

Accession	Sequence	Position
D6	33421 AAATTATCATTAATTAATGTATGTTTTTAAATTTATATGAAAACTGCTATTATAGTA	33562
QY	173 GTTGCAAGAGAACATGAAAGGCAAAATATAACGATGAAACCATTACTAGCTTTGGCTGT	232
D6	33361 TCTGGATTACTTAATTTTATCTATATATATGTAATAATGAAATTATTCATTGTTAGCAATA	33302
QY	233 ATCAGACCAATTAACCTGAAATGCACTGTGCTAGCAATGCTAAGTATTAAGAAAGGTAGC	292
D6	33301 ATAAATTCATTATTAATTAATAATTAATAATTAATAGTTATTTATTAATAATATGTAATAT	33242
QY	293 ATGGAGATCTATATTATTTTGGCTAAGCTCTTAAGTACAT	336
D6	33241 AATACAAATATATATAAATAATATATATATTAATTAATTTCCAT	33198

Search completed: February 12, 2006, 00:05:55
Job time : 182 secs

Search completed: February 12, 2006, 00:05:55
Job time : 182 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:30:15 ; Search time 3911 Seconds

(without alignments)
9374.591 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAGAGTCATTCATTCGCTT.....TGTTCATGTCATGAGGCTGC 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_dr:*
9: gb_to:*
10: gb_str:*
11: gb_gy:*
12: gb_un:*
13: gb_vl:*
14: gb_hlg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	645	100.0	6550	6	BD132692 Regulator
2	645	100.0	6550	6	AR208995 Sequence
3	645	100.0	6550	6	AR482064 Sequence
4	645	100.0	9335	6	BD132709 Regulator
5	645	100.0	9335	6	AR209012 Sequence
6	645	100.0	9335	6	AR482081 Sequence
7	46.2	7.2	2000	6	AX655393 Sequence
8	45.8	7.1	12028	2	AE001412 Sequence
9	44.4	6.9	13383	2	AE001374 Plasmid
10	44.4	6.9	128666	5	BX510935 Zebrafish
11	43.8	6.8	138363	6	CQ869722 Sequence
12	43.8	6.8	210331	8	AL157402 Human DNA
13	42.8	6.6	1525	2	AY701198 Orconecte
14	42.8	6.6	50000	6	AX392733 Sequence
15	42.8	6.6	232392	13	AF250284 Ambacta m
16	42.2	6.5	155952	8	AC004534 Homo sapi
17	42	6.5	183246	14	AC118486 Rattus no
18	41.8	6.5	92620	15	AB026636 Arabidops

19	41.8	6.5	153232	5	AL772263 Zebrafish
20	41.8	6.5	158330	8	AC025599 Homo sapi
21	41.8	6.5	195070	14	AC068995 Homo sapi
22	41.6	6.4	127270	8	AC004740 Homo sapi
23	41.6	6.4	196260	14	AC136415 Rattus no
24	41.6	6.4	246134	14	AC135647 Rattus no
25	41.4	6.4	157811	8	AC079071 Homo sapi
26	41.4	6.4	168500	14	AC021796 Homo sapi
27	41	6.4	69471	14	AC117400_3 Continuation (106
28	41	6.4	110000	15	AP008218_105 Continuation (106
29	41	6.4	112916	15	CNS08C9X
30	41	6.4	130672	15	CNS08C9Z
31	41	6.4	147359	8	AP002345 Homo sapi
32	40.8	6.3	1055	6	AR579681 Sequence
33	40.8	6.3	1055	6	AX083745 Sequence
34	40.8	6.3	75589	8	BS000034 Pan trogl
35	40.8	6.3	145274	8	AC113559 Homo sapi
36	40.6	6.3	348034	2	CR382400 Plasmid
37	40.6	6.3	704	10	BV475571 GS91P6310
38	40.6	6.3	1522	2	AY701231 Orconecte
39	40.6	6.3	155935	8	AC006442 Homo sapi
40	40.6	6.3	157028	8	AL139000 Human DNA
41	40.6	6.3	225038	14	AC111507 Rattus no
42	40.6	6.3	236550	14	AC103061 Rattus no
43	40.4	6.3	97751	8	AC084257 Homo sapi
44	40.4	6.3	155821	8	AC027043 Homo sapi
45	40.4	6.3	169262	8	AC090569 Homo sapi

ALIGNMENTS

RESULT 1	BD132692	6550 bp	DNA	linear	PAT 18-SEP-2002
LOCUS	BD132692	Regulatory sequences for transgenic plants.			
DEFINITION	BD132692	Regulatory sequences for transgenic plants.			
ACCESSION	BD132692	Regulatory sequences for transgenic plants.			
VERSION	BD132692.1	GI_23227637			
KEYWORDS	JP 2002504824-A/1.				
SOURCE	JP 2002504824-A/1.				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 6550)				
AUTHORS	Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N., Wenke,M.A., Parreddy,D., Petolino,V.F., Smith,K. and Woosley,A.				
TITLE	Regulatory sequences for transgenic plants				
JOURNAL	Patent: JP 2002504824-A 1 12-FEB-2002;				
COMMENT	DOM AGROSCIENCES LLC				
	PN JP 2002504824-A/1				
	PD 12-FEB-2002 JP 199503094				
	PF 10-JUN-1998 JP 199503094				
	PR 12-JUN-1997 US 60/049752				
	PI MICHAEL AINLEY, KATHERINE ARMSTRONG, SCOTT BELMAR, OTTO FOLKERTS, PI NICOLE HOPKINS, MICHAEL A MENKE, DAYAKAR PARREDDY, JOSEPH F PI PETOLINO.				
	PI KELLEY SMITH, AARON WOOSLEY				
	PC C12N15/53, C12N15/82, A01H5/00				
	CC Strandness: Double;				
	CC Topology: Linear;				
	CC /products='peroxidase'				
	FT Key	Location/Qualifiers			
	FT exon	4201..4425			
	FT intron	4426..5058			
	FT exon	5059..5250			
	FT intron	5251..5382			
	FT exon	5383..5548			
	FT intron	5549..5649			
	FT exon	5650..6065			
	FT CDS				
	FT join(4201..4425,5059..5250,5383..5547,5649..6068)				
FEATURES	Location/Qualifiers				
source	1..6550				

ORIGIN

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 100.0%; Score 645; DB 6; Length 6550;
Best Local Similarity 100.0%; Pred. No. 8.6e-134;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 60
DB 4420 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 4479
QY 61 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 120
DB 4480 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 4539
QY 121 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 180
DB 4540 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 4599
QY 181 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 240
DB 4600 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 4659
QY 241 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 300
DB 4660 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 4719
QY 301 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 360
DB 4720 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 4779
QY 361 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 420
DB 4780 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 4839
QY 421 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 480
DB 4840 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 4899
QY 481 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 540
DB 4900 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 4959
QY 541 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 600
DB 4960 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 5019
QY 601 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 5064

RESULT 2
LOCUS AR208995 6550 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6384207.
ACCESSION AR208995
VERSION AR208995.1 GI:21510295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6550)
AUTHORS Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.
TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6384207-A 1 07-MAY-2002;
FEATURES Location/Qualifiers
1..6550
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 645; DB 6; Length 6550;
Best Local Similarity 100.0%; Pred. No. 8.6e-134;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 60
DB 4420 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 4479
QY 61 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 120
DB 4480 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 4539
QY 121 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 180
DB 4540 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 4599
QY 181 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 240
DB 4600 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 4659
QY 241 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 300
DB 4660 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 4719
QY 301 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 360
DB 4720 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 4779
QY 361 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 420
DB 4780 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 4839
QY 421 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 480
DB 4840 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 4899
QY 481 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 540
DB 4900 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 4959
QY 541 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 600
DB 4960 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 5019
QY 601 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 5064

RESULT 3
LOCUS AR482064 6550 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 1 from patent US 6699964.
ACCESSION AR482064
VERSION AR482064.1 GI:47244032
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6550)
AUTHORS Ainley,M., Armstrong,K., Belmar,S., Folkerts,O., Hopkins,N.,
Menke,M.A., Pareddy,D., Petolino,J.F., Smith,K. and Woosley,A.
TITLE Regulatory sequences for transgenic plants
JOURNAL Patent: US 6699964-A 1 02-MAR-2004;
FEATURES Location/Qualifiers
1..6550
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 645; DB 6; Length 6550;
Best Local Similarity 100.0%; Pred. No. 8.6e-134;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 60
DB 4420 GTCAAGGTCATATTCCTCTCCCTGTGTATGCTTATATTCATAGCTCTGCAAGCT 4479
QY 61 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 120
DB 4480 ATAAAGCTTGATCTGCAATATATATTAACAAGTTAGCTACACAAGTTTGTACTTCAAG 4539
QY 121 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 180
DB 4540 TCTTTTAATATATGTTGGTGAATATAGATTATGATATCCATATGAAAGTGTTCAG 4599
QY 181 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 240
DB 4600 AGAACAATGAAAGGCAAAAGATTAACCGATGAACCATTTACTAGCTTGGCTGTATCAGACC 4659
QY 241 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 300
DB 4660 AATTAATCTGAAATGCACTTGTGTAGCATGCTTAAGTATTAAGAAAGTATGAGAGA 4719
QY 301 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 360
DB 4720 ATCTATATATATTTTGGCTAACTTCTTTAGTTACTATTAATGATGAAGAACCTTACCATT 4779
QY 361 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 420
DB 4780 GCCCATGCGCAGCCCTAATGTCCTGGTGAACATGATGCGCAATGATGATTAATTACT 4839
QY 421 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 480
DB 4840 CTATTTGTTCTCTTTTGAAGTGTGTATTAAGATGTCCTTTTGAAGCATCTGAGAG 4899
QY 481 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 540
DB 4900 ATGTTTAACTTAACCTTAAGTGGCAATGATGATGAGCTCTCAGTGCAACGCAATGCTCTGT 4959
QY 541 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 600
DB 4960 AATCTACTGTCAACCACTACTGTGATGATGCTTAACCTTAACCTTAACCTTAACCTTAACCT 5019
QY 601 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 645
DB 5020 AGTAATTAACCAATCAATTAACAACACTGTTAACATGATGAGGCTGC 5064


```
/note="AT_rich"
/rpt_type=tandem
1569..1617
repeat_region
/rpt_type=tandem
complement(1569..1617)
/rpt_type=tandem
/rpt_unit="(ta)n"
repeat_region
complement(1726..1858)
/note="AT_rich"
/rpt_type=tandem
complement(1757..1810)
/rpt_type=tandem
/rpt_unit="(ta)n"
1761..1810
repeat_region
/rpt_type=tandem
complement(<1855..>4521)
/locus_tag="PFB0695c"
mRNA
complement(<1855..>4521)
/locus_tag="PFB0695c"
complement(1855..4521)
/locus_tag="PFB0695c"
CDS
/codon_start=1
/product="acyl-CoA synthetase"
/protein_id="PAC71928.1"
/db_xref="GI:3845253"
/translaction="MHIIISVCLFIYIIHVPCKSGCLGDKGYSEICKAIYENES
NTRCKMDHLREBLFIYKPKLLKKYRLRNKKIAIVEHAYGEPONFITYGKPRKV
LSFSGHINNEGSGIOGSKYKHOHNGWPLLGIVSGSNINMLIVDMAAMSGVTLL
LHNSPSIDVYVNLNTEKLEWLCDDIDVUGLLHREHPYLKLLIDNLYPRIID
ILRYFNNENNVSEYDASDDSDSSSEFINDGLAIVDEKLEKIDLERKKN
VGIRLFEPDVSSVPTKYNQIDBPDFTISIVTSGTSGKPGVWLSINMYNALVP
LCGSHMLNHPKAHLSTLPVSHYERNVVAALSGIKIDIMSKNINFSRDLFENSG
ELIAYGVKFNRIYLSINMAEINMLSATKRNIKNVPSLRSVACAFYMLBGLTYS
SLRNCVNPVLLEVLNCGGKLSPIAEELVILNANPYOGYGLTEITGPIFYQCKDY
NTSISGPIAPNPKYKRYTETKASDSTPKGELLKSDIPKGYELERLTNSSTY
DHFVTEGDIQINDNSLTFLDRSKGLVKLSQSGYLETDLNNTISIPINCCVYG
DRLDEALATISVDKYLFRCLRDNNMLNTEGINKNMYMDKSDONINTKHFLDYKN
KMLEVYNNTLNINYNIIINHYLTSKTWDITNVLPTMKVRFVIODYAFIDOVNI
FKKLGQOKERTKLOKTSDEOIKNDENDOKSKSYPSRLOSOKRSQSKENKST
SOEKNSIOEKKSKSKKXKNTSLPDNINISIPVQNKIEKPOQNNNSNITLKTTLKST
DASLKIPKRNKVTNKSFRVOVQVRELEENS"
2056..2151
repeat_region
/rpt_type=tandem
complement(2056..2147)
/rpt_type=tandem
/rpt_unit="(caaa)n"
repeat_region
complement(2284..2312)
/note="AT_rich"
/rpt_type=tandem
complement(2409..2462)
/note="AT_rich"
repeat_region
/rpt_type=tandem
complement(4305..4326)
/note="AT_rich"
/rpt_type=tandem
complement(4561..4594)
/rpt_type=tandem
/rpt_unit="(ta)n"
repeat_region
complement(4615..4664)
/note="AT_rich"
/rpt_type=tandem
complement(4742..4888)
/rpt_type=tandem
/rpt_unit="(ta)n"
4893..5076
repeat_region
/rpt_type=tandem
/rpt_unit="(caaaa)n"
4977..5049
repeat_region
/rpt_type=tandem
4977..5048
repeat_region
/rpt_type=tandem
complement(4977..5048)
/rpt_type=tandem
```

```
/rpt_unit="(ta)n"
repeat_region
complement(5187..5279)
/rpt_type=tandem
/rpt_unit="(ta)n"
repeat_region
complement(5304..5331)
/note="AT_rich"
/rpt_type=tandem
complement(5358..5400)
/rpt_type=tandem
/rpt_unit="(ta)n"
5361..5400
repeat_region
/rpt_type=tandem
5410..5455
repeat_region
/rpt_type=tandem
/rpt_unit="(a)n"
complement(5471..5545)
/rpt_type=tandem
/rpt_unit="(ta)n"
5474..5545
repeat_region
/rpt_type=tandem
complement(5581..5648)
/note="AT_rich"
/rpt_type=tandem
complement(5661..5720)
/rpt_type=tandem
/rpt_unit="(a)n"
complement(5749..5788)
/note="AT_rich"
/rpt_type=tandem
5776..5842
repeat_region
/rpt_type=tandem

Query Match 7.1%; Score 45.8; DB 2; Length 12028;
Best Local Similarity 46.4%; Pred. No. 3.2;
Matches 149; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

11 AATTGCTCTCTCTGTATGTTCTTATATTAATGATGCTGTGCAAGCTATTAAGCTTG 70
1530 AATTAAATTTATGAGAAATCTAGAGAAATAAATGTTATTAATATTAATTAAT 1589
71 ATATCGACATTAATTAACAAGTTAGCTACACAAGTTTTGTACTCAAGCTTTTAACT 130
1590 ATATATATATATATATATATATATATATATATTAAGAAAGTTATTTATGATATTAAT 1649
131 ATATGTTGGTCAATTAAGATTAGATAATCCATATGAAGTGTGCAAGAACTGAA 190
1650 ATTAAGTTCCCATTTATATTAATTTGTGAAGCTATATTTCTTACAAAATAATGCAA 1709
191 AGGCAAAATTAAGGATGAACCATTAAGCTTGGCTGTATGAGACCAATTAAGTTGA 250
1710 AAAAATTAATATGAGGAAATATATTAATATGATATATGTAATTAAGATACATATATATA 1769
251 AATGCACTGTGTACATGCTTAAGTATTAAGAAAGTATGAGGAAATCTATATTA 310
1770 AATATATTCATATATATATATATATATATATATATATATATATATATATTTT 1829
311 TTTGGCTAACCTCTTAAGTT 331
1830 GATTATTTGATATTTTGT 1850

RESULT 9
AE001374 1383 bp DNA linear INV 04-OCT-2002
LOCUS AE001374 AE001362
DEFINITION complete sequence.
ACCESSION AE001374.1 GI:3845100
VERSION AE001374.1
KEYWORDS
SOURCE Plasmodium falciptarum 3D7
ORGANISM Plasmodium falciptarum 3D7
REFERENCE Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 13383)
```

<p>AUTHORS</p> <p>JOURNAL</p> <p>REFERENCE</p> <p>AUTHORS</p>	<p>Gardner,M.J., Tetteijn,H., Carucci,D.J., Cummings,L.M., Aravind,L., Koonin,E.V., Shallow,S., Mason,T., Yu,K., Fujii,C., Pedersen,J., Shen,K., Jing,J., Aston,C., Lai,Z., Schwartz,D.C., Ferreira,M., Salzb erg,S., Zhou,L., Sutton,G.G., Clayton,R., White,O., Smith,H.O., Fraser,C.M., Adams,M.D., Venter,J.C. and Hoffman,S.L. Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum</p> <p>Science 282 (5391), 1126-1132 (1998)</p> <p>2 (bases 1 to 13383)</p> <p>Gardner,M.J., Hall,N., Pung,B., White,O., Berriman,M., Hyman,R.W., Carlton,J.M., Paul,A., Nelson,K.E., Bowman,S., Paulsen,I.T., James,K., Bisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A., Kyes,S., Chan,M.-S., Nene,V., Shallow,S.J., Suh,B., Peterson,J., Angiolini,S., Perlea,M., Allen,J., Selengut,J., Haft,D., Mather,M.W., Valdya,A.B., Martin,D.M.A., Fairhead,A.H., Fraunholz,M.J., Roos,D.S., Ralph,S.A., McPadden,G.I., Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C., Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and Barrall,B.</p> <p>Genome sequence of the human malaria parasite Plasmodium falciparum Nature 419, 498-511 (2002)</p> <p>3 (bases 1 to 13383)</p> <p>Gardner,M.J.</p> <p>Direct Submission</p> <p>Submitted (02-OCT-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA</p> <p>Location/Qualifiers</p>	<p>1. .13383</p> <p>/organism="Plasmodium falciparum 3D7"</p> <p>/mol_type="genomic DNA"</p> <p>/isolate="3D7"</p> <p>/db_xref="taxon:36329"</p> <p>/chromosome="2"</p> <p>27. .70</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>45. .70</p> <p>/rpt_type=tandem</p> <p>complement(88. .127)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(ca)n"</p> <p>complement(167. .318)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>319. .349</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>complement(356. .420)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(443. .482)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(503. .551)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(ca)n"</p> <p>503. .550</p> <p>/rpt_type=tandem</p> <p>complement(627. .676)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>683. .712</p> <p>/rpt_type=tandem</p> <p>complement(683. .712)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(cataa)n"</p> <p>816. .845</p> <p>/rpt_type=tandem</p> <p>complement(816. .845)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>complement(884. .1033)</p>	<p>/rpt_type=tandem</p> <p>/rpt_unit="(cataa)n"</p> <p>complement(1078. .1102)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(1151. .1172)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(ta)n"</p> <p>complement(1226. .1254)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>complement(1257. .1297)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(1331. .1596)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>1532. .1567</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(taaa)n"</p> <p>complement(1694. .1772)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(1773. .1795)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(caaaa)n"</p> <p>complement(1817. .1841)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(taaaa)n"</p> <p>1847. .1905</p> <p>/rpt_type=tandem</p> <p>complement(1847. .1905)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(taaaa)n"</p> <p>complement(1906. .2070)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>1978. .2012</p> <p>/rpt_type=tandem</p> <p>complement(2130. .2171)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p><2176. .>2496</p> <p>/locus_tag="PF0120w"</p> <p><2176. .>2496</p> <p>/locus_tag="PF0120w"</p> <p>2176. .2496</p> <p>/locus_tag="PF0120w"</p> <p>/codon_start=1</p> <p>/product="hypothetical protein"</p> <p>/protein_id="AAC71814.1"</p> <p>/db_xref="GI:3845101"</p> <p>/translation="MKLSKILYFALLALNFIAPRDYNSWYAKPKLTPAERKKRNONIMYSSIASAVALLIGAVGLGHLHKNKNGDKKGTGPAKKDNDKNAVNSISSTMYRA"</p> <p>2555. .2596</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>2567. .2596</p> <p>/rpt_type=tandem</p> <p>complement(2666. .2695)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(a)n"</p> <p>2828. .2884</p> <p>/rpt_type=tandem</p> <p>complement(2832. .2888)</p> <p>/rpt_type=tandem</p> <p>/rpt_unit="(ta)n"</p> <p>complement(2917. .2968)</p> <p>/note="AT_rich"</p> <p>/rpt_type=tandem</p> <p>complement(3012. .3053)</p> <p>/note="AT_rich"</p>
---	---	--	--

Query Match	6.9%	Score 44.4	DB 2	Length 13383
Best Local Similarity	57.5%	Pred. No. 6.4	71	Indels 3
Matches 100	Conservative 0	Mismatches		Gaps 1
Qy	19	TTCTCTGTATGTTCTTTATATTAACATGCTCTGCAAGAGCTATTAAGAGCTTGATACGCA	78	
Db	3507	TTATATATTTTATATTTTAAATCCCATATTCAGATTAATACAAATTTTGA--TTCA	3563	
Qy	79	GATATAATTAACAAGTACGACACAAGTTTGTACTCTCAAGTCTTTAACTATATGTTG	138	
Db	3564	GAATTAATTTTAATATTTTCTTTTACAAATTTTAACTATATATTTTAAATTAATATTA	3623	
Qy	139	GTGCAATTAAGATTATGAGTAATCCATATGAAAGTGTTCAGAGAACTGAAG	192	
Db	3624	CTGTATTCATTCATTGATTAACAAATATGACCGTTTCAAGATACGTCGACG	3677	
RESULT 10				
LOCUS	BX510935	128666 bp	DNA	linear VRT 25-JUL-2005
DEFINITION	Zebrafish DNA sequence from clone DK51-207124 in linkage group 14,			
ACCESSION	BX510935			
VERSION	BX510935.28	GI:71142384		
KEYWORDS	HTG.			
SOURCE	Danio rerio (zebrafish)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

```

REFERENCE
AUTHORS
TITLE
JOURNAL

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 128666)

Direct Submission
Submitted (23-JUL-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests:
http://www.sanger.ac.uk/projects/vertebrate/faq.shtml#databases
On Jul 23, 2005 this sequence version replaced gi:62719292.

-----
Center: Wellcome Trust Sanger Institute
Genome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk

-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL, Sw, SWISSPROT, Tr, TREMBL, Wp, WORMPEP, Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
Clone-derived Zebrafish pUC subclones occasionally display
inconsistency over the length of mononucleotide A/T runs and
conserved TA repeats. Where this is found the longest good quality
representation will be submitted.
Any regions longer than 1kb tagged as misc-feature 'unsure' are
part of a tandem repeat of more than 10kb in length where it has
not been possible to anchor the base differences between repeat
copies. The region has been built up based on the repeat element
to match the total size of repeat indicated by restriction digest,
but repeat copies may not be in the correct order and the usual
finishing criteria may not apply.
DKEY-207L24 is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5.

location/Qualifiers
1.128666
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/chromosome="14"
/clone="DKEY-207L24"
/clone_1lb="Dantiokey"

ORIGIN

Query Match 6.9%; Score 44.4; DB 5; Length 128666;
Best Local Similarity 49.6%; Pred. No. 3.4;
Matches 114; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

121 TCTTTTACTATATGTTGGTGCATTAAGATTATGAGTAATCCATATGAAAGGTTGCCAG 180
2575 TTTTTTAAAAAGTAATAATTACTGTAAAGTTTAAAGCTGCCAAATACAAAGAGTGCAAA 72516
181 AGAAGATGAAGAAAGAAAGATTAACGATGAAGAACCACTTACAGCTTGGCGTATCGAC 240
72515 ATACACACACACAAAAAAAACCTGATTAACACACACACATTAATTAATTACCAATAT 724566
241 AATAACTTGAAGTCACTTGTGCATGATCCCTAAGATTTAGAAAAGTAGCATGGGAGA 300
72455 AATAAGATGCAATGTTAACTCTACACTGATTTATTTTAAAGTAAGTTGCCAAAGATT 723996
301 ATCTAATATATTGGCTAACTTCTTTAGTACTATGATGATGAGAA 350
72395 ATTTTCAATTCAGATAGATTTCATTTGTTGTCTCTTTAGAAATTAATA 72346

RESULT 11

```


[illegible]

of Pieter de Jong. For further details see
http://www.chori.org/dacpac/home.htm
VECTOR: pBACE3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
Location/Qualifiers
1. 210331
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="q31.2-q31.3"
/clone="RP11-553K8"
/clone_1lb="RPCT-11.2"
1
/note="Clone left end: RP11-553K8"
complement(join(8379..8721,14238..14338,21836..21881,
25726..25842,26032..26102))
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-002"
complement(join(8379..8721,14238..14338,21836..21881,
25726..25842,26032..26102))
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-002"
/product="ATPase, H+ transporting, lysosomal 13kDa, V1
subunit G isoform 3"
/note="match: ESTs: Em:AI733150.1 Em:AI766184.1
Em:AI792793.1 Em:AI831521.1 Em:AW612374.1 Em:AW614583.1
Em:BF195729.1 Em:BF197645.1 Em:BF509031.1"
complement(join(8379..8721,14238..14338,25726..25892))
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
complement(join(8379..8721,14238..14338,25726..25892))
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
/product="ATPase, H+ transporting, lysosomal 13kDa, V1
subunit G isoform 3"
/note="match: ESTs: Em:AI635711.1 Em:AI733453.1
Em:BX114684.1
match: cDNAs: Em:AY039760.1"
complement(8379)
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
complement(8382)
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
complement(8394..8399)
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
complement(join(8548..8721,14238..14338,25726..25807))
/gene="ATP6V1G3"
/locus_tag="RP11-553K8.1-001"
/note="match: proteins: Sw:Q96LBP4 Tr:QB8MC1"
/codon_start=1
/product="ATPase, H+ transporting, lysosomal 13kDa, V1
subunit G isoform 3"
/protein_id="CA15638.1"
/db_xref="GI:55957706"
/db_xref="InterPro:IPR005124"
/translation="WTSQSGIHQLQAEGRADKLEBAKIRGKRLKQKEANWEI
DGRKDRDKFRLKQSKINGSQNNLSDELSEDTLGKIQELNGHYNNKYMESVNNQLISM

```
misc_feature
VCDKPEIHVNRATN"
45222..45313
/note="Sequence from clone PCR only."
gene
complement(join(82881..83140,83923..84025))
/locus_tag="RP11-553K8.2-001"
mRNA
complement(join(82881..83140,83923..84025))
/locus_tag="RP11-553K8.2-001"
/product="novel transcript"
gene
/note="match: ESTs: Em:BU568146.1"
join(123828..123855,124383..124498,177503..177529,
188454..188528,189628..189654,191890..192108,
193289..193313)
/gene="PTPRC"
/locus_tag="RP11-553K8.4-011"
/locus_tag="protein tyrosine phosphatase, receptor type, C"
/note="match: ESTs: Em:CD687228.1"
join(124197..124294,124383..124498,177503..177529,
181868..182065,184720..184860,187543..187686,
188454..188528,189628..189654,191890..192108,
193289..193417,194843..194960,198109..198228,
201838..201996,203250..203458,207572..207632,
AL355988.7:5165..5273,AL355988.7:5962..5996,
AL355988.7:8442..8551,AL355988.7:9125..9215,
AL355988.7:9305..9381,AL355988.7:11021..11057,
AL355988.7:11153..11250,AL355988.7:11952..12077,
AL355988.7:18694..18851,AL355988.7:19057..19192,
AL355988.7:20879..21028,AL355988.7:24934..25024,
AL355988.7:26241..26374,AL355988.7:27317..27451,
AL355988.7:29074..29196,AL355988.7:29419..29597,
AL355988.7:31094..31229,AL355988.7:32731..34108)
/gene="PTPRC"
/locus_tag="RP11-553K8.4-001"
/locus_tag="protein tyrosine phosphatase, receptor type, C"
/note="match: ESTs: Em:AA309577.1 Em:AA317100.1
Em:AI500108.1 Em:AV171515.1 Em:AW23710.1 Em:AY00082.1
Em:AM503474.1 Em:BE719688.1 Em:BF901880.1 Em:BS54357.1
Em:BO003526.1 Em:BU429842.1 Em:BX643527.1 Em:CS15613.1
Em:CD686097.1 Em:CD689696.1 Em:CD690467.1 Em:CD691504.1
Em:CD692375.1 Em:CD695545.1 Em:CD696557.1 Em:CD699227.1
Em:CD707896.1 Em:H10346.1
match: CDNA5: Em:Y00638.1"
join(124252..124294,124383..124498,177503..177529,
188454..188528,189628..189654,191890..192108,
193289..193417,194843..194960,198109..198228,
201838..201996,203250..203458,207572..207632,
AL355988.7:5165..5273,AL355988.7:5962..5996,
AL355988.7:8442..8551,AL355988.7:9125..9215,
AL355988.7:9305..9381,AL355988.7:11021..11057,
AL355988.7:11153..11250,AL355988.7:11952..12077,
AL355988.7:18694..18851,AL355988.7:19057..19192,
AL355988.7:20879..21028,AL355988.7:24934..25024,
AL355988.7:26241..26374,AL355988.7:27317..27451,
AL355988.7:29074..29196,AL355988.7:29419..29597,
AL355988.7:31094..31229,AL355988.7:32731..34108)
/gene="PTPRC"
/locus_tag="RP11-553K8.4-001"
/product="protein tyrosine phosphatase, receptor type, C"
/note="match: ESTs: Em:AA309577.1 Em:AA317100.1
Em:AI500108.1 Em:AV171515.1 Em:AW23710.1 Em:AY00082.1
Em:AM503474.1 Em:BE719688.1 Em:BF901880.1 Em:BS54357.1
Em:BO003526.1 Em:BU429842.1 Em:BX643527.1 Em:CS15613.1
Em:CD686097.1 Em:CD689696.1 Em:CD690467.1 Em:CD691504.1
Em:CD692375.1 Em:CD695545.1 Em:CD696557.1 Em:CD699227.1
Em:CD707896.1 Em:H10346.1
match: CDNA5: Em:Y00638.1"
join(124252..124294,124383..124498,177503..177529,
188454..188528,189628..189654,191890..192108,
193289..193417,194843..194960,198109..198228,
201838..201996,203250..203458,207572..207632,
AL355988.7:5165..5273,AL355988.7:5962..5996,
AL355988.7:8442..8551,AL355988.7:9125..9215,
AL355988.7:9305..9381,AL355988.7:11021..11057,
AL355988.7:11153..11250,AL355988.7:11952..12077,
AL355988.7:18694..18851,AL355988.7:19057..19192,
AL355988.7:20879..21028,AL355988.7:24934..25024,
AL355988.7:26241..26374,AL355988.7:27317..27451,
AL355988.7:29074..29196,AL355988.7:29419..29597,
AL355988.7:31094..31229,AL355988.7:32731..34108,
AL355988.7:26241..26374,AL355988.7:27317..27451,
```

```
mRNA
AL355988.7:29074..29196,AL355988.7:29419..29597,
AL355988.7:31094..31229,AL355988.7:32731..34108)
/gene="PTPRC"
/locus_tag="RP11-553K8.4-002"
/locus_tag="protein tyrosine phosphatase, receptor type, C"
/note="match: ESTs: Em:AI374817.1 Em:AI673089.1
Em:AI765195.1 Em:CD683888.1 Em:CD688449.1 Em:CD697158.1
Em:CD699512.1"
Query Match 6.8%; Score 43.8; DB 8; Length 210331;
Best Local Similarity 53.1%; Pred. No. 4.1;
Matches 93; Conservative 0; Mismatches 82; Indels 0; Gaps 0;
QY 37 TATATTACATGCTCTGACCAAGCTATTAAGCTGATCTGACATATATTAACAAGTTA 96
DB 183066 TCTTGACTTGCTGTGAGGACGACGACATTTATTTAAGTCTGATATACCAATA 183007
QY 97 GCTACCAAGTTTGTGACTTCAAGCTTTTAACTATATGTTGGCAATAGATTATGAG 156
DB 183006 ACTTCATGATGATGATCAATCAAAATCTTGAATGATCCCTTAACAAATTTCTGATGG 182947
QY 157 TAATCATATGAAGCTGTTCAGAGAACATGAAAGCAAGTAATACGATGAA 211
DB 182946 TATTATATATGCTTGTGTTTCAACAGAAATATGATGTTTAAACAGTTCAA 182892
RESULT 13
AY701198 1525 bp DNA linear INV 15-FEB-2005
LOCUS AY701198
DEFINITION Orconectes indianensis cytochrome oxidase subunit I-like (COI)
ACCESSION AY701198
VERSION AY701198.1 GI:58917844
KEYWORDS mitochondrion Orconectes indianensis
SOURCE Orconectes indianensis
ORGANISM Orconectes indianensis
REFERENCE 1 (bases 1 to 1525)
AUTHORS Taylor,C.A. and Knouff,J.H.
TITLE Historical influences on genital morphology among sympatric crayfishes: systematics and gonopod evolution in the genus Orconectes (Cambaridae)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1525)
AUTHORS Taylor,C.A. and Knouff,J.H.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-2004) CBD, INHS, 607 E. Peabody Dr., Champaign, IL 61820, USA
FEATURES
location/Qualifiers
1..1525
/organism="Orconectes indianensis"
/mol_type="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:306148"
<1..1525
/gene="COI"
```



```
CDS      2273. .2545
          /gene="AMVTR03"
          /codon_start=1
          /product="AMVTR03"
          /protein_id="AG02975.1"
          /db_xref="GI:9944792"
          /translation="MNANEDMLNEIYIKLDNYSIYVDKDLINGIANDKINKESNNYL
          LKSMEDCKLIEMSYNYSKDSLELEIKLLANTFELAKYIQQNK"
          complement (2542. .2934)
          /gene="AMVTR04"
          complement (2542. .2934)
          /gene="AMVTR04"
          /codon_start=1
          /product="AMVTR04"
          /protein_id="AG02987.1"
          /db_xref="GI:9944804"
          /translation="MEWLLILPSFIICCPKOSKPFCDIYPCINNLMKSCNNE
          VRNNCTITSEYKNITGNVCHRCNKXILLPGIHYNPLMCKNLSNWCCEBDNYIY
          CTEQNKYIWKDYNTDCKSIIEKICY"
          complement (2971. .3786)
          /gene="AMVTR05"
          complement (2971. .3786)
          /gene="AMVTR05"
          /codon_start=1
          /product="AMVTR05"
          /protein_id="AG02988.1"
          /db_xref="GI:9944805"
          /translation="MDYERLNNRLSTPONDYKXYISIIILIIILIIICYLIF
          AKESNTNDSKTIINIKIYSNNWVYDDEFKALIRYNTKINKNSEEQIPEIA
          RSRITSLYNNITDIIDYRCGVNDNKKMIIDEMCDYDINVYVYRLNCDNISR
          EIONSPFMYENYIMFENSEKNYIDIDYCVNNNNPFGMYKNNKIIINLKTILSL
          KYEYHMLSHIFIKHDFILNSYTFPIEYNDKNIDEERIYMFKNINHCY"
          3871. .4416
          /gene="AMVTR06"
          3871. .4416
          /gene="AMVTR06"
          /codon_start=1
          /product="AMVTR06"
          /protein_id="AG02978.1"
          /db_xref="GI:9944795"
          /translation="MDPIKQDIARISITDNLNIPIGARKINKNVFNCMPFNN
          OIICNYCKLCSGCNKLNNLSIKRFSTKGYRENNKFNILLCDICKNTEICIECH
          KLFYNNNIDYVBLRNTDSIODKVGCKFCLINLDCENRYLTNTYINSYNNNYL
          FRYENDEFNNYKICIREYI"
          complement (4597. .4872)
          /gene="AMVTR07"
          complement (4597. .4872)
          /gene="AMVTR07"
          /codon_start=1
          /product="AMVTR07"
          /protein_id="AG02989.1"
          /db_xref="GI:9944806"
          /translation="MDSIKSTSTTKSTDLSEIYSNTTDSIKSTSTIKSTDTTDSID
          LINPTSTIKSTDTTIDINDESTIKSTINITSKDYKQWKYFLK"
          complement (5363. .6939)
          /gene="AMVTR08"
          complement (5363. .6939)
          /gene="AMVTR08"
          /codon_start=1
          /product="AMVTR08"
          /protein_id="AG02990.1"
          /db_xref="GI:9944807"
          /translation="MNIIKICKILFGLIFVFTIIIIYHNITNNNDEYDIRNITEYK
          IIKYKKNIDINNEYLKNKDLSEIIEPESSTIKSTDTTDPKSTDSIKSTDLSEIYS
          NTDSTIKSTSTIKSTDLSEIISNTTBSIKSTSTIKSTDLSEIISNTTBSMBSIKST
          DSTIKSTDLSEIISNTTDSIKSTSTIKSTDLSEIISNTTBSMDSIKSTDLSEIISNTTDSIK
          STSTIKSTDLSEIISNTTDSMDSIKSTSTIKSTDLSEIISNTTDSIKSTDLSEIISNTTDSIKST
          DLSEIISNTTDSIKSTSTIKSTDLSEIISNTTDSIKSTDLSEIISNTTDSIKSTDLSEIISNTTDS
          IDSIKSTSTIKSTDLSEIISNTTDSIKSTSTIKSTDLSEIISNTTDSIKSTDLSEIISNTTDSIKSTDS
          TIKSTDLSEIISNTTDSIKSTSTIKSTDLSEIISNTTDSIKSTSTIKSTDLSEIISNTTDSIKSTDLSEIIS
          KYLSDSIKST"
          7018. .7224
          gene
```

```
CDS      /gene="AMVTR09"
          7018. .7224
          /gene="AMVTR09"
          /codon_start=1
          /product="AMVTR09"
          /protein_id="AG02981.1"
          /db_xref="GI:9944798"
          /translation="MKRIQVIGPNNLTLANIQIISINKTYAKTTIENNRPHVFDL
          LVNYPTEPFIILTNKQEEYWRPMI"
          7248. .7748
          /gene="AMVTR10"
          7248. .7748
          /gene="AMVTR10"
          /codon_start=1
          /product="AMVTR10"
          /protein_id="AG02982.1"
          /db_xref="GI:9944799"
          /translation="MKRIQVIGPNNLTLANIQIISINKTYAKTTIENNRPHVFDL
          VFYIKTRPFRITYESYIGVPIENNERYIRIYNTTEKLFPAEPLGRLLIYDKAGE
          LFFPINVIYIMNLSLKIYDAVAILTNINYNLFLYVFIPIFIYIYIYINRKQVL
          KKNIN"
          7783. .8163
          /gene="AMVTR11"
          7783. .8163
          /gene="AMVTR11"
          /codon_start=1
          /product="AMVTR11"
          /protein_id="AG02983.1"
          /db_xref="GI:9944800"
          /translation="MSVNNINNYDNKICIDCYRKYKQNEINKKIQPDLILFIQYLF
          VLISITLTYIITLCIENPKIQYIILLCYILMIGIYSIVAKIDKENATISFLI
          DVCKKRHRSSLPYTESLWPDV"
          complement (8177. .8737)
          /gene="AMVTR12"
          complement (8177. .8737)
          /gene="AMVTR12"
          /codon_start=1
          /product="AMVTR12"
          /protein_id="AG02991.1"
          /db_xref="GI:9944808"
          /translation="MDXYIINGFITIPSOIGNEYDCLNKIKIONHIVNNNTID
          GYIHIDKIIYITNKKYKXGNNNITKYEINIRIINIPYDSKKNKVSCKKCK
          YDYICKINDNETIPVDLNPDTVINSSNIIYECDDNIRDPNKVGMSKYLISIIIL
          IILIIILRFYIKKIFHAYESVR"
          complement (8798. .8992)
          /gene="AMVTR13"
          complement (8798. .8992)
          /gene="AMVTR13"
          /codon_start=1
          /product="AMVTR13"
          /protein_id="AG02992.1"
          /db_xref="GI:9944809"
          /translation="MYGDEKGTQMYENIHKYDNBYILFYTTQDEPKHISKDKIDNEN
          DVFKNLTININIKYKTDPR"
          9826. .10068
          /gene="AMV001"
          9826. .10068
          /gene="AMV001"
          /codon_start=1
          /product="AMV001"
          /protein_id="AG02707.1"
          /db_xref="GI:9944524"
          /translation="MDFSIIKTNFMIIEPIFIISVGSIMISIANENGLMIISNI
          SSIAFYKKQYVLCQQCVFLLTIIIGIYVMDKL"
          10272. .10703
          /gene="AMV002"
          10272. .10703
          /gene="AMV002"
          /note="putative dufPase"
          /codon_start=1
          Query Match      6.6%; Score 42.8; DB 13; Length 232392;
          Best Local Similarity 45.9%; Pred. No. 6.7;
```

Matches 146; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Oy	27	TTATGCTCTTAATATATACATGCTGTGCAAGAGCTATPAAAGCTTGATATGCAAGATATAA	86
Db	11134	TGATATTAATATGTAATATTAATTAATGTATATTTCTATPAAAGTATAAATAATTTTGAATTTAA	11075
Oy	87	TAAACAAGTTAGCTACACAAGTTTGTGACTTCAAGTCTTTTAATCTATATGTGGTGCAATA	146
Db	11074	TAAATTAATATTAATAAAGAAACAGATTTTATCTGTAATATTTTAATTTTACAAAAAGTATATC	11015
Oy	147	AGATTATGAGTAAATCCATATGAAAGTGTGCAAGAGACATGAAGGCAAGATTAACCG	206
Db	11014	TTATTAATCCGATGTTTGCAAAACAGATTTGAAAAAAATACAAATATATATATATATGT	10955
Oy	207	ATGAACCCATTACTAGCTTTGGCTGTATCAGACCAATAACTGAAATGCACTTGTCTAG	266
Db	10954	AAATATTAATATTTCCGATTTCTTTGTATGTATTAATTTAAAAAGAAATATTTATGCAA	10895
Oy	267	CATCCCTTAAGATTAAGAAAAGTAGCATGGGAGATCTATATATTTTGGCTAACTTCTT	326
Db	10894	CAATACAGTAATAATATATATACGTTATTAATAAAAATTATMAATGTTATATATATACAAA	10835
Oy	327	TAGTTACTATGATTGAT 344	
Db	10834	AAAGTTATATATTTTCAT 10817	

Search completed: February 11, 2006, 23:44:43
Job time : 3916 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:25:29 ; Search time 556 Seconds

(Without alignments)
7731.523 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645

Sequence: 1 GTCAGAGTCATTCATTCGCTT.....TGTTCATGTCGTCAGGCTGC 645

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_21.*
1: Geneseqn19908.*
2: Geneseqn19908.*
3: Geneseqn20008.*
4: Geneseqn20018.*
5: Geneseqn20018.*
6: Geneseqn20028.*
7: Geneseqn20028.*
8: Geneseqn20038.*
9: Geneseqn20038.*
10: Geneseqn20038.*
11: Geneseqn20038.*
12: Geneseqn20048.*
13: Geneseqn20048.*
14: Geneseqn20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	645	100.0	1682	12	ADJ48190	Adj48190 Maize oil
2	645	100.0	6550	2	AAV63737	AAV63737 Maize, per
3	645	100.0	9335	2	AAV63734	AAV63734 Plasmid p
4	557	86.4	709	12	ADJ48004	Adj48004 Maize oil
5	47.6	7.4	1119	12	ADJ48213	Adj48213 Maize oil
6	47.6	7.4	2000	11	ACU35363	ACU35363 Rice stre
7	46.2	7.2	2000	8	ADA71938	Ada71938 Rice gene
8	43.8	6.8	138363	13	ABD32624	ABD32624 Human can
9	42.8	6.6	2000	11	ACU35363	ACU35363 Rice stre
10	42.8	6.6	50000	6	ABL55643	ABL55643 AmpV gen
11	40.2	6.2	10710	6	ABL32893	ABL32893 Human imm
12	40.2	6.2	19459	6	ABK31213	ABK31213 Signal tr
13	40.2	6.2	19459	6	ABL70528	ABL70528 Chemical
14	40.2	6.2	33053	6	ABO67006	ABO67006 Human ang
15	40.2	6.2	40862	6	ABL34072	ABL34072 Human imm
16	39.6	6.1	2000	8	ADA71938	Ada71938 Rice gene
17	39.6	6.1	5376	6	ABL34150	ABL34150 Human imm
18	39.4	6.1	83391	6	ABO67093	ABO67093 Human ang
19	39.2	6.1	2890	12	ADG63901	ADG63901 Novel hum

C	20	39.2	6.1	3531	12	ADG63920	Adg63920 Novel hum
C	21	39.2	6.1	4782	8	ACC44434	Acc44434 Gene enco
C	22	39.2	6.1	5052	12	ADG64457	Adg64457 Novel hum
C	23	39.2	6.1	6145	12	ADG22133	Adg22133 Human sof
C	24	39.2	6.1	8757	10	ADD29766	Add29766 Human tum
C	25	38.8	6.0	7134	6	ABL32483	AbL32483 Human imm
C	26	38.8	6.0	10467	6	ABK28454	Abk28454 DNA trans
C	27	38.6	6.0	5930	6	ABL32517	AbL32517 Human imm
C	28	38.6	6.0	7108	6	ABK39996	Abk39996 Human che
C	29	38.6	6.0	9905	6	ABL32062	AbL32062 Human imm
C	30	38.6	6.0	10329	6	ABL34122	AbL34122 Human imm
C	31	38.6	6.0	10886	6	ABL34134	AbL34134 Human imm
C	32	38.6	6.0	13511	6	ABL32281	AbL32281 Human imm
C	33	38.6	6.0	18512	6	ABL32977	AbL32977 Human imm
C	34	38.2	5.9	19707	6	ABL33420	AbL33420 Human imm
C	35	37.6	5.8	2000	11	ACU37108	ACU37108 Rice stre
C	36	37.6	5.8	38596	10	ADG63503	Adg63503 Mycoplaem
C	37	37.6	5.8	38596	10	ACC69133	Acc69133 Mycoplaem
C	38	37.6	5.8	38596	12	ADN48938	Adn48938 Mycoplaem
C	39	37.6	5.8	50000	6	ABL56201	AbL56201 AmpV gen
C	40	37.6	5.8	110000	2	AAT58840_4	Continuation (5 of
C	41	37.2	5.8	567	14	ADV74973	Adv74973 Human col
C	42	37.2	5.8	787	2	AAZ16598	Aaz16598 Human gen
C	43	37.2	5.8	1724	12	ADN05537	Adn05537 Antipsoxi
C	44	37.2	5.8	1726	9	ACH04267	Ach04267 Human CDN
C	45	37.2	5.8	1844	2	AAZ24588	Aaz24588 Human lun

ALIGNMENTS

RESULT 1	ADJ48190	standard, DNA; 1682 BP.
ID	ADJ48190	
XX	ADJ48190;	
AC		
XX		
DT	06-MAY-2004	(first entry)
XX		
DE	Maize oil-associated gene #8.	
XX		
KW	de; maize; plant; oil-associated gene; transgenic; enhanced seed oil;	
KM	vegetable oil.	
XX		
OS	Zea mays.	
XX		
PN	US2004025202-A1.	
XX		
PD	05-FEB-2004.	
XX		
PF	14-MAR-2003; 2003US-00389566.	
XX		
PR	15-MAR-2002; 2002US-0365301P.	
PR	26-JUN-2002; 2002US-0391786P.	
PR	26-JUN-2002; 2002US-0392018P.	
XX		
PA	(LAUR/ LAURIE C. C.	
PA	(RAVA/ RAVANELLO M.	
PA	(SAVA/ SAVAGE T.	
PA	(LEDE/ LEDEAUX J R.	
PA	(ROGE/ ROGERS J A.	
XX		
PI	Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;	
XX		
XX	WPI; 2004-142683/14.	
DR		
XX		
PT	Novel recombinant DNA construct comprising a promoter functional in	
PT	plants operably linked to an oil-associated gene for producing transgenic	
PT	plant seed.	
XX		
PS	Example 1; SEQ ID NO 194; 22pp; English.	
XX		
CC	The invention relates to a recombinant DNA construct comprising a	


```
FT /note= "sequence from pB1221"
FT 3'UTR 4280..4652
FT /*tag= 1
FT /note= "perts 3'UTR"
FT misc_feature 4653..4869
FT /*tag= 3
FT /note= "synthetic linker"
FT misc_feature 4870..5121
FT /*tag= k
FT /note= "CamV DNA nt 7093-7344"
FT misc_feature 5122..5129
FT /*tag= 1
FT /note= "linker"
FT misc_feature 5130..5476
FT /*tag= m
FT /note= "CamV DNA nt 7093-7439"
FT misc_feature 5477..5496
FT /*tag= n
FT /note= "linker"
FT misc_feature 5497..5606
FT /*tag= o
FT /note= "maize streak virus synthetic leader (MSV nt 167-186, 188-277)"
FT intron 5608..5698
FT /*tag= p
FT /note= "Adh1.S nt 119-209"
FT intron 5699..5820
FT /*tag= q
FT /note= "Adh1.S nt 555-672 plus 4-base linker"
FT misc_feature 5828..5864
FT /*tag= r
FT /note= "maize streak virus nt 278-317"
FT CDS 5865..6419
FT /*tag= s
FT /product= "phosphinothricin acetyltransferase gene"
FT /note= "Basta resistance selectable marker"
FT 3'UTR 6420..6699
FT /*tag= t
FT /note= "nos 3'UTR"
FT misc_feature 6700..9335
FT /*tag= u
FT /note= "pUC19 sequences"
XX MO9856921-A1.
XX 17-DEC-1998.
XX 10-JUN-1998; 98MO-US011921.
XX 12-JUN-1997; 97US-0049752P.
XX (DOWC ) DOW AGROSCIENCES LLC.
XX Ainsley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
XX Parredy D, Petolino JF, Smith K, Woosley A;
XX WPI, 1999-080904/07.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (perts) gene.
XX
XX Example 17; Page 117-122; 150pp; English.
XX
XX This is the nucleotide sequence of PIGP/367, a plasmid containing the
XX maize root preferential cationic peroxidase perts gene (see (see AAV63717)
XX promoter, the perts untranslated leader modified to include the perts intron
XX 1, the GUS gene, and the perts 3' untranslated region (3'UTR). Because
XX intron flanking sequences (exon DNA) are important in the processing of
XX the intron, 16 bases of flanking exon DNA were included in the fusion
XX within the perts untranslated leader. Transformation experiments in maize
XX demonstrated that the presence of the perts intron is essential for root-
XX specific expression from the perts promoter. The invention relates to
```

CC Isolated regulatory sequences, especially promoter, intron and 3'UTR
CC sequences, of the maize perts gene. Claimed recombinant gene cassettes
CC comprising perts regulatory sequences are used to control expression of
CC recombinant genes in selected tissue, especially the root, of transformed
CC plants, particularly maize

SQ Sequence 9335 BP; 2402 A; 2290 C; 2258 G; 2385 T; 0 U; 0 Other;

Query Match 100.0%; Score 645; DB 2; Length 9335;
Best Local Similarity 100.0%; Pred. No. 2,3e-166;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GTCAAGTTCOAATTCCTGCTTCCTGTTATGTTCTTATATTCATGCTCTGCAAAAGCT 60
DB 1758 GTCAAGTTCOAATTCCTGCTTCCTGTTATGTTCTTATATTCATGCTCTGCAAAAGCT 1817
QY 61 ATTAAGCTTGATACGCACTATTAATTAACAAGTTGCAACAACTTTTGTACTCAAG 120
DB 1818 ATTAAGCTTGATACGCACTATTAATTAACAAGTTGCAACAACTTTTGTACTCAAG 1877
QY 121 TCTTTTAACTATATGTTGGTGCATATAGATTATAGATTAATCCATATGAAGTGTGCAAG 180
DB 1878 TCTTTTAACTATATGTTGGTGCATATAGATTATAGATTAATCCATATGAAGTGTGCAAG 1937
QY 181 AGAATCATGAAGCAAAAGATTAACGAGTAAACCATTAAGCTTTGCTGTATCAAGCC 240
DB 1938 AGAATCATGAAGCAAAAGATTAACGAGTAAACCATTAAGCTTTGCTGTATCAAGCC 1997
QY 241 AATTAATTTGAATGCACTGTTGTGATGATGCTTAATTAATTAAGTATGAGGAGA 300
DB 1998 AATTAATTTGAATGCACTGTTGTGATGATGCTTAATTAATTAAGTATGAGGAGA 2057
QY 301 ATCTATATTTATTTGGCTAATCTCTTAATTAATTAATTAATTAATTAATTAATTAAT 360
DB 2058 ATCTATATTTATTTGGCTAATCTCTTAATTAATTAATTAATTAATTAATTAATTAAT 2117
QY 361 GCCCATGCAAGCCCTAATGTCCTCGGTGACATGATGACCAAGTACTATGATTAATTTACT 420
DB 2118 GCCCATGCAAGCCCTAATGTCCTCGGTGACATGATGACCAAGTACTATGATTAATTTACT 2177
QY 421 CTAATGTCCTCCTTTTATAGTGTGATTAAGTATGCTTTTATAGCCACGCAAG 480
DB 2178 CTAATGTCCTCCTTTTATAGTGTGATTAAGTATGCTTTTATAGCCACGCAAG 2237
QY 481 ATGTTACTTAACTAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
DB 2238 ATGTTACTTAACTAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2297
QY 541 AATCTACTGTGACCACTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 2298 AATCTACTGTGACCACTACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2357
QY 601 AGTAATTAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 645
DB 2358 AGTAATTAACCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2402
RESULT 4
ADJ48004
ID ADJ48004 standard; DNA; 709 BP.
XX
XX AC ADJ48004;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Maize oil-associated gene genomic amplicon #8.
XX
XX KW ds; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
XX vegetable oil.
XX
XX OS Zea mays.
XX
XX PN US2004025202-A1.
```

```

XX 05-FEB-2004.
PD 14-MAR-2003; 2003US-00389566.
XX 15-MAR-2002; 2002US-0365301P.
XX 26-JUN-2002; 2002US-0391786P.
XX 26-JUN-2002; 2002US-0392018P.
XX (LAUR/) LAURIE C. C.
XX (RAVA/) RAVANELLO M.
XX (SAVA/) SAVAGE T.
XX (LEDE/) LEDEAUX J. R.
XX (ROGE/) ROGERS J. A.
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX Example 1; SEQ ID NO 8; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene genomic amplicon.
XX Sequence 709 BP; 203 A; 141 C; 155 G; 210 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 557; DB 12; Length 709;
XX Best Local Similarity 99.1%; Pred. No. 1.4e-142;
XX Matches 560; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX
XX 81 ATATATTAACAGTAGCTACACAGTTTGTACTTCAAGCTTTTAACTATATGTTGT 140
XX 1 ACATATTAACAGTAGCTACACAGTTTGTACTTCAAGCTTTTAACTATATGTTGT 60
XX 141 GCAATTAAGATTAGTAATCCATATGAGAGTGTGCAAGAGAAATGAAAGCAAGAT 200
XX 61 GCAATTAAGATTAGTAATCCATATGAGAGTGTGCAAGAGATGAAAGCAAGAT 120
XX 201 AAACGATGAACCCATTACTAGCTTGGCTGTATCAAGCAATTAATCTGAAATGCACTTG 260
XX 121 AAACGATGAACCCATTACTAGCTTGGCTGTATCAAGCAATTAATCTGAAATGCACTTG 180
XX 261 TGTAGTACCTCTAAGTATTAGAAAAGTAGCATGGAGAAATCTATATTTTGGCTAA 320
XX 181 TGTAGTACCTCTAAGTATTAGAAAAGTAGCATGGAGAAATCTATATTTTGGCTAA 240
XX 321 CTTCCTTAAGTATTAGTATGAGAAAAGCTTACCATTTGCCATGCCAGCCCTAATGT 380
XX 241 CTTCCTTAAGTATTAGTATGAGAAAAGCTTACCATTTGCCATGCCAGCCCTAATGT 300
XX 381 CCGGATGACATGATTGAGCCAGTACTATGATTAATTAATTAATCTATGTTCTCTTTTGA 440
XX 301 CCGGATGACATGATTGAGCCAGTACTATGATTAATTAATTAATCTATGTTCTCTTTTGA 360
XX 441 GTGCTGTATTAAGATGCTCTTTTGTGAGCACTGAGAAAGTGTATTAATCTTAAGT 500
XX 361 GTGCTGTATTAAGATGCTCTTTTGTGAGCACTGAGAAAGTGTATTAATCTTAAGT 420
XX 501 CGCAATGATTGAGCTCTGAGTCAAGCATGCTCTGTATTAATCTTAAGTCAACTACT 560
XX 421 CGCAATGATTGAGCTCTGAGTCAAGCATGCTCTGTATTAATCTTAAGTCAACTACT 480

```

```

XX 561 CTGATGATGCTGCTTAACCTTAACCTATTCACGAGGCTAGTAAATTAACATCACTTAC 620
XX 481 CTGATGATGCTGCTTAACCTTAACCTATTCACGAGGCTAGTAAATTAACATCACTTAC 540
XX 621 AACACTGTTAATCAATGATGAGGCTGC 645
XX 541 AACACTGTTAATCAATGATGAGGCTGC 565
XX
XX RESULT 5
XX ADJ48213
XX ID ADJ48213 standard; DNA; 1119 BP.
XX AC ADJ48213;
XX DT 06-MAY-2004 (first entry)
XX DE Maize oil-associated gene #31.
XX KW de; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
XX vegetable oil.
XX Zea mays.
XX US2004025202-A1.
XX 05-FEB-2004.
XX 14-MAR-2003; 2003US-00389566.
XX 15-MAR-2002; 2002US-0365301P.
XX 26-JUN-2002; 2002US-0391786P.
XX 26-JUN-2002; 2002US-0392018P.
XX (LAUR/) LAURIE C. C.
XX (RAVA/) RAVANELLO M.
XX (SAVA/) SAVAGE T.
XX (LEDE/) LEDEAUX J. R.
XX (ROGE/) ROGERS J. A.
XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX Example 1; SEQ ID NO 217; 22pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene.
XX Sequence 1119 BP; 279 A; 283 C; 265 G; 292 T; 0 U; 0 Other;
XX
XX Query Match 7.4%; Score 47.6; DB 12; Length 1119;
XX Best Local Similarity 85.5%; Pred. No. 0.011;
XX Matches 53; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX 584 AACTATTCACGAGGCTAGTAATTAACATCACTTACACACGCTTAAGGCT 643
XX 15 AACAGTATGACACACAGTAATTAACATCACTTACACACGCTTAAGGCT 74
XX 644 GC 645
XX 75 GC 76

```

```
RESULT 6
ACLS35363/C
ID ACL35363 standard, cDNA; 2000 BP.
XX
XX ACL35363;
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Rice stress-regulated promoter SEQ ID NO:13926.
DE
XX
XX sb; abiotic stress tolerance; transgenic plant; plant; cereal;
KM
XX
XX Oryza sativa.
XX
XX WO2003008540-A2.
XX
XX 30-JAN-2003.
XX
XX 21-JUN-2002; 2002MO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX
XX 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN ) SYNGENRA PARTICIPATIONS AG.
XX
XX Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Rieke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 48; SEQ ID NO 13926; 899p; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 2000 BP; 540 A; 344 C; 416 G; 428 T; 0 U; 272 Other;
SQ
Query Match 7.4%; Score 47.6; DB 11; Length 2000;
Best Local Similarity 15.6%; Pred. No. 0.013;
Matches 56; Conservative 145; Mismatches 159; Indels 0; Gaps 0;
QY 104 AAGTTTGACTCTCAAGCTTTTAAGTAATGTTGGTGCATATAGATTATGATCA 163
DB 369 AAGTCGTTTASGCMWTKTMMKTKMAAKAMAWYMYSHRYRMYYSW 310
QY 164 TATGAAGCTGTTCAGAGAAACATGAAGCAAGATAACGATGAACCCATTACAC 223
DB 309 AAWGAGWRWSKTBARBSMAWTKWAKWYBAVSKWKKKWWYTBAAWATMTMM 250
QY 224 TTTCGGCTGATCAGACCAATCACTTGAATGCACTTGTGCTGACATGCCCTTAAGATTA 283
DB 249 TMMWARKWTRYMAMKWTYAAWMTYAAWAAWTAATATMTKATGAAWMTWMSWAGWAAAKWY 190
```

```
QY 284 AAAGTAGCATGGAGAAATCTATATTATTTGGCTACTCTTTAGTACTATGATGA 343
DB 189 WTKRYWTRBARAGMYRRTMKMTSMCTMMWMMWMTTWTYWRKAKRKARGATGW 130
QY 344 TGAGAAAGCCTTACCATGGCCATGCGCATATATCTCCGGTGAATGATGACCA 403
DB 129 WWRKYAMSWTWTJKRKMYMKRTMRWKYCCRAAMWSWCTYSWMMWYKSTWSKMSGS 70
QY 404 ACTATGATTAATTACTCTATGTTCTCCCTTTTGTAGTGTGATATAGATGCTTTT 463
DB 69 AGTMTKYAKYMMTRMTKTRKTRISWKAAMWTCCKRKATCMKMMKKMMWYKTYT 10
RESULT 7
ADA71938/C
ID ADA71938 standard, DNA; 2000 BP.
XX
XX ADA71938;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Rice gene, SEQ ID 5263.
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
KM
XX
XX gene; ds.
XX
XX Oryza sativa.
XX
XX WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001MO-IB001105.
XX
XX 22-JUN-2001; 2001MO-IB001105.
XX
XX (SYGN ) SYNGENRA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 27; SEQ ID NO 5263; 899p; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
XX Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
SQ
Query Match 7.2%; Score 46.2; DB 8; Length 2000;
Best Local Similarity 12.2%; Pred. No. 0.031;
Matches 63; Conservative 225; Mismatches 218; Indels 11; Gaps 1;
QY 12 ATTCTGCTTCCTGTATGTTCTTTATATATATCATGCTGTGACAAAGCTATAAGCTTGA 71
DB 987 WKRYWAKRYAMWSRKTWCTGKBAATYGTCTMAAGRRWRWAMCMYCCMMWCMW 928
QY 72 TACTGAGTAAATATATAACAAGTTAGCTACAAAGTTTGTACTTCAAGTCTTTAACTA 131
```


Db 10834 AAGTATATATTTTCAT 10817

RESULT 11

ABL32893
ID ABL32893 standard; DNA; 10710 BP.

XX
AC ABL32893;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 866.

XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antiasthma; cytosine methylation; antiasthmatic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antineoplastic; antineoplastic; antidiabetic; antidiabetic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.

XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIC-) EPIDENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.

XX
PS Claim 1; SEQ ID NO 866; 32pp + Sequence listing; German.

XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention

XX
SQ Sequence 10710 BP; 3653 A; 81 C; 1963 G; 5013 T; 0 U; 0 Other;

Query Match 6.2%; Score 40.2; DB 6; Length 10710;
Best Local Similarity 50.3%; Pred. No. 2.4;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 63
DB 10207 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 10266

QY 64 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 123
DB 10267 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 10326

QY 124 TTAACTATATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 183
DB 10327 TTAACTATATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 10386

QY 184 ACATGAAGGCAAGAT 200

Db 10387 AGTTAAATATGATTAAT 10403

RESULT 12

ABK31213
ID ABK31213 standard; DNA; 19459 BP.

XX
AC ABK31213;
XX
DT 23-APR-2002 (first entry)
XX
DE Signal transduction associated gene modified complementary DNA #28.

XX
KW Human; signal transduction associated gene; cytosine methylation state;
KW CpG island; signal transduction associated disease; solid tumour; cancer;
KW antitumour; cytosine; mutant; ds.

XX
OS Homo sapiens.
XX
PN WO200200926-A2.
XX
PD 03-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-EP007472.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIC-) EPIDENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-147896/19.
XX
PT Oligonucleotide for diagnosis and therapy of diseases associated with
PT signal transduction e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with signal transduction.

XX
PS Claim 1; SEQ ID NO 56; 24pp; English.

XX
CC The present invention relates to chemically modified DNA sequences of
CC signal transduction associated genes. The DNA sequences are chemically
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting
CC the cytosine methylation state (CpG islands) of these genes, and a method
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of
CC genes associated with signal transduction. The genomic DNA can be
CC obtained from cells or cellular components which contain DNA, e.g. cell
CC lines, biopsies, blood, sputum, stool, urine, cerebral spinal fluid,
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,
CC brain, heart, prostate, lung, breast or liver, histologic object slides,
CC and all their possible combinations. The sequences of the invention are
CC useful for the diagnosis and therapy of diseases associated with signal
CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent
CC chemically pretreated genomic DNA sequences of different genes associated
CC with signal transduction, or their complementary sequences. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office

XX
SQ Sequence 19459 BP; 6064 A; 245 C; 3866 G; 9284 T; 0 U; 0 Other;

Query Match 6.2%; Score 40.2; DB 6; Length 19459;
Best Local Similarity 50.3%; Pred. No. 2.9;
Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 4 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 63
DB 4986 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 5045

QY 64 AAGGTCATTCCTGCTCTGTTATGTTCTTATATTCATGCTCTGCAAGCTAT 123

	5046	124	5106	184	5166
Db	AGGTTTAAACGTTAGATTATAAATAATTTAGACGAAAATTTAGGTATATATAT	TTTACTATATGTTGGTCAAATAAGATTATAGTAATTCATATAGAAAGGTGTTGCAGAGA	TTAGAGATTATAGTAGTGGTAAAGAAATTTATGTTTAAATAATTAAAGTAATGTAATAAA	ACATGAAAGGCAAGAT 200	AGTTAAATTTGATAAAT 5182
Qy					
Db					
Qy					
Db					

RESULT 13
ABL70528
ID ABL70528 standard; DNA; 19459 BP.

DE Chemically treated cell signaling DNA sequence complementary to#209.

KW Cell signalling; cytosine methylation; cell signalling disease; cancer;
KW tumour; cytosstatic; ds.

OS Unidentified

PN WO200202807-A2.

PD 10-JAN-2002.

PF 29-JUN-2001; 2001WO-EP007471.

PR 30-JUN-2000; 2000DE-01032529.

PR 01-SEP-2000; 2000DE-01043826.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-154758/20.

PT Nucleic acid, useful for diagnosis and therapy of diseases associated
PT with cell signaling e.g. cancer, comprises chemically modified genomic
PT sequences of genes associated with cell signaling.

PS Claim 1; SEQ ID NO 418; 24pp + Sequence Listing; English.

CC The invention relates to a nucleic acid comprising a sequence of at least
CC 18 bases of a segment of chemically pretreated DNA of genes associated
CC with cell signalling. The activity of the modified sequences of the
CC invention may be described as cytostatic. The object of the invention is
CC to provide the chemically modified DNA of genes associated with cell
CC signalling, as well as oligonucleotides and/or RNA-oligomers for
CC detecting cytosine methylations, as well as a method which is
CC particularly suitable for the diagnosis and/or therapy of genetic and
CC epigenetic parameters of genes associated with cell signalling. The
CC chemically modified DNA provided by the invention is useful for diagnosis
CC and therapy of diseases such as solid tumours and cancer. The sequences
CC given in records ABL/7011-ABL/70626 represent chemically pre-treated
CC genomic DNA's of genes associated with cell signalling. Note: The
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office

Sequence 19459 BP; 6064 A; 245 C; 3866 G; 9284 T; 0 U; 0 Other;

Query Match	6.28;	Score 40.2;	DB 6;	Length 19459;
-------------	-------	-------------	-------	---------------

Matches 99; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

4 AAGGTTCAATCTGCTTCCCTGTATGTTCTTTATATTACATGCTTGACAAAGCTATA 63

A vertical ruler with markings from 0 to 10 cm. The markings are in millimeters, with major ticks every centimeter and minor ticks every millimeter. The ruler is oriented vertically with the 0 mark at the top and the 10 cm mark at the bottom.

Dd	4886	AAGCTTGAATGGATTTTTTTTATTATTTTAATAAATAATTAATTTAAAGTGGATTAA	5045
Qy	64	AAGCTTGATACTCGATPAATATATPACAAGTTAGCTACACAGAATTTGTACTTCAAGTCT	123
Dd	5046	AGGTTTAACGCTTAGATTTAAAAATTATPAAAAATTTTGAAGAAAATTTAGCTAATTAATAT	51050
Qy	124	TTTAACTATATGTTGCGCAATAGATTATGAGTATCCATATGAAGTGTTCGAAAGGA	183
Dd	5106	TTAGAGATATAGTATGGGTAAAGGATTTATGTTTAAATATTTAAAGTAAAGGTAAATAAA	51655
Qy	184	ACATGAAGCGCAAAGAT	200
Dd	5166	AGTTAAAAATTGATTAAT	5182

RESULT 14
ABQ67006
ID ABQ67006 standard; DNA; 33053 BP.

DT 28-AUG-2002 (first entry)

DE Human angiogenesis associated polynucleotide SEQ ID NO 36.

KW Human angiogenesis; methylation; eye disease; glaucoma; tumour;
 KW inflammation; rheumatoid arthritis; diabetic retinopathy; anticancer
 KW macular degeneration; inflammatory bowel disease; Crohn's disease;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiarteriosclerotic; ds.

OS Homo sapiens.

PN WO200246454-A2.

PD 13-JUN-2002.

PF 06-DEC-2001; 2001WO-EP014320.

PR 06-DEC-2000; 2000DE-01061338.

PA (EPiG-) EPIGENOMICS AG.

PI Schacht O;

DR WPI; 2002-500450/53.

PT New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer.

PS Claim 1; SEQ ID NO 36; 41pp + Sequence Listing; German.

The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiodysgenesis-associated genes (II) having sequences (ABQ65971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiodysgenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriatic, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 33053 BP; 10862 A; 283 C; 6271 G; 15637 T; 0 U; 0 Other;

Query Match 6.28; Score 40.2; DB 6; Length 33053;

Matches	99;	Conservative	0;	Mismatches	98;	Indels	0;	Gaps	0.
---------	-----	--------------	----	------------	-----	--------	----	------	----

4 AAGGTTCAATTCTGCTTCTCTGTATGTTCTTTATATTACATGCTCTGACAAAGCTATA 63

THIS PAGE BLANK (USPTO)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 11, 2006, 22:39:35 ; Search time 3703 Seconds
(without alignments)
8149.519 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645

Sequence: 1 GTCAGGTCGATTCGCTT.....TGTTCATGTCGAGGCTGC 645

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	625	96.9	973	10	CG154041 PUFZS22TB
2	603	93.5	819	9	CC642795 OGWDI19TV
3	517.2	80.2	994	10	CG154043 PUFZS22TD
4	383.8	59.5	872	8	CK607568 AVR1.29.B
5	382.4	59.3	432	10	CG042359 PULI085TB
6	259	40.2	800	9	CC642785 OGWDI19TV
7	226.6	35.1	975	10	CG155200 PUKC047B
8	77	11.9	734	9	CC400812 PUBGX18TD
9	75.4	11.7	886	10	CG031509 PUFZS22TB
10	73.6	11.4	858	10	CG311059 OG5CY43TC
11	49.8	7.4	345	9	CC721634 OG2AD27TH
12	47.6	7.4	597	8	DN487904 R014B11.3
13	42.8	6.6	754	10	CL180658 104_390_1
14	41.8	6.5	375	3	BP526721 BP526721
15	41.8	6.5	684	9	CC950911 BOIR08TF
16	41.6	6.4	650	6	CD293786 SCDPUS36.
17	41.4	6.4	539	9	CC156622 1014e03.b
18	41.4	6.4	638	10	CG142220 PUFZS22TB
19	40.8	6.3	441	1	AL383889 MCBC17E04
20	40.8	6.3	444	8	R39925 YF51e09.81
21	40.6	6.3	347	9	BH473918 BOHNU33TR
22	40.6	6.3	773	9	B2236858 CH230-333

C	23	40.6	6.3	933	10	CNS00CFN	AL059220 Drosophila
C	24	40.6	6.3	1101	10	CNS0039G	AL063921 Drosophila
C	25	40.4	6.3	360	1	AL464043	AL464043 A3464043
C	26	40.4	6.3	1101	10	CNS00FMC	AL070972 Drosophila
C	27	40.4	6.3	1101	10	CNS0106X	AL058595 Drosophila
C	28	40.2	6.2	600	9	AQ395724	AQ395724 CIRBI-E1-
C	29	40.2	6.2	612	9	AQ390717	AQ390717 CIRBI-E1-
C	30	40.2	6.2	615	3	B1351457	B1351457 B1351457
C	31	40.2	6.2	658	3	B1342361	B1342361 B1342361
C	32	40.2	6.2	789	9	BZ606212	BZ606212 WHACB56TF
C	33	40.2	6.2	813	10	CZ703754	CZ703754 OC_Ba002
C	34	40.2	6.2	832	3	BM333797	BM333797 50072-2-1
C	35	40	6.2	747	10	AG605701	AG605701 Mus muscu
C	36	39.8	6.2	650	9	CC870062	CC870062 NDL.22D6
C	37	39.8	6.2	967	10	CNS000UP	AL070653 Drosophila
C	38	39.6	6.1	604	10	CE428277	CE428277 E1gr-g88-
C	39	39.6	6.1	809	9	AZ670202	AZ670202 ENTJ167TF
C	40	39.6	6.1	877	9	AZ547430	AZ547430 ENTJ167TF
C	41	39.6	6.1	975	5	B0711132	B0711132 AGENCOURT
C	42	39.6	6.1	985	10	CNS00CFN	AL058780 Drosophila
C	43	39.6	6.1	987	10	CNS014PQ	AL104456 Drosophila
C	44	39.4	6.1	491	10	CZ633677	CZ633677 OM_Ba017
C	45	39.4	6.1	1040	9	BZ463282	BZ463282 BONKO17TR

ALIGNMENTS

RESULT 1
LOCUS CG154041 973 bp DNA linear GSS 21-AUG-2003
DEFINITION PUFZS22TB_ZM_0.6_1.0_KB_Zea mays genomic clone ZMBR10770C19,
genomic survey sequence.
ACCESSION CG154041 GI:34044842
VERSION CG154041.1
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Bennett, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Rennett, A., 1997. The Zm1.0 genome project: a high-resolution
map of the maize genome.

AUTHORS

Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Bennett, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Rennett, A., 1997. The Zm1.0 genome project: a high-resolution
map of the maize genome.

TITLE

Unpublished (2003)

JOURNAL

Other GSS: PUFZS22TD

COMMENT

Contract: Cathy Whitelaw
TIGR Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. 973
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBR10770C19"
/note="Vector: PCR4-TOPO, Site 1: EcoRI, 0.6-1.0 kb high
COT selected genomic DNA library"

FEATURES

source
1. 973
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBR10770C19"
/note="Vector: PCR4-TOPO, Site 1: EcoRI, 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 96.9%; Score 625; DB 10; Length 973;
Best Local Similarity 99.1%; Pred. No. 5.1e-154;
Matches 639; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
1 GTCAGGTCGATTCGCTTCTGTATGTTCTTATATTCATGCTGCAAGCT 60

Db 47 GTCAAGGTCGAATCTCTCTCTGTAGTCTTATATATACATCTCTGACAA-CT 105
QY 61 ATTAAGCTTATCTGAGATATAATATACAGTACTCTACAGAGTTTGACTTCAAG 120
Db 106 ATTAAGCTTATCTGAGATATAATATACAGTACTCTACAGAGTTTGACTTCAAG 165
QY 121 TCTTTTAATAATATGTTGTCATTAAGATTATAGTAATACATATGAGTGTGCAAG 180
Db 166 TCTTTTAATAATATGTTGTCATTAAGATTATAGTAATACATATGAGTGTGCAAG 225
QY 181 AGAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTGGCTGTACAGACC 240
Db 226 CGAATATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTGGCTGTACAGACC 285
QY 241 AATACTGAAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGGTGCAAGTGGAGA 300
Db 286 AATACTGAAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGGTGCAAGTGGAGA 345
QY 301 ATCTATATTAATTTGGCTAACTTCTTAACTTATGATTAAGTAAGAAAGCTTACCAT 360
Db 346 ATCTATATTAATTTGGCTAACTTCTTAACTTATGATTAAGTAAGAAAGCTTACCAT 405
QY 361 GCCCATGCCAGCCCTTAATGTCGGGTGACATGATTAAGCACTATGATTAATTTACT 420
Db 406 GCCCATGCCAGCCCTTAATGTCGGGTGACATGATTAAGCACTATGATTAATTTACT 465
QY 421 CTATGTTCTCTCTTTTGAAGTGTGTAAGATGCTTTTGAAGCACTGCAAG 480
Db 466 CTATGTTCTCTCTTTTGAAGTGTGTAAGATGCTTTTGAAGCACTGCAAG 525
QY 481 ATGTTTACTTAATCTAGTGTGCAATGATTAAGTGAAGCTCTAGTGAACGATGCTGT 540
Db 526 ATGTTTACTTAATCTAGTGTGCAATGATTAAGTGAAGCTCTAGTGAACGATGCTGT 585
QY 541 AATCTACTGTACACACTACTGTGTGTGTGCTTAACTCTTAACTATTCACGTGCT 600
Db 586 AATCTACTGTACACACTACTGTGTGTGTGCTTAACTCTTAACTATTCACGTGCT 645
QY 601 AGTAATACCAATCATTTACACACTGTGTATCATGTGTGAGGCTGC 645
Db 646 AGTAATACCAATCATTTACACACTGTGTATCATGTGTGAGGCTGC 690

RESULT 2
CC642795 819 bp DNA linear GSS 19-JUN-2003
LOCUS OGM019TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZM5BMA0555C14,
DEFINITION CC642795 genomic survey sequence.
ACCESSION CC642795
VERSION CC642795.1 GI:32028363
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
AUTHORS 1 (bases 1 to 819)
White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Frazer, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nuneberg, A., Robbins, D. and Lake, J.A.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OGM019TH
Contact: Cathy White,law
TIIGR
7912 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: white,law@cihr.org
Seq primer: TF
Class: methylation filtered.
FEATURES Location/Qualifiers

source 1. .819
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5BMA0555C14"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

Query Match 93.5%; Score 603; DB 9; Length 819;
Best Local Similarity 98.8%; Pred. No. 3, 2e-148;
Matches 639; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 1 GTCAAGGTCGAATCTCTCTCTGTAGTCTTATATATACATCTCTGACAA-CT 60
Db 158 GTCAAGGTCGAATCTCTCTCTGTAGTCTTATATATACATCTCTGACAA-CT 216
QY 61 ATTAAGCTTATCTGAGATATAATATACAGTACTCTACAGAGTTTGACTTCAAG 120
Db 217 ATTAAGCTTATCTGAGATATAATATACAGTACTCTACAGAGTTTGACTTCAAG 276
QY 121 TCTTTTAATAATATGTTGTCATTAAGATTATAGTAATACATATGAGTGTGCAAG 180
Db 277 TCTTTTAATAATATGTTGTCATTAAGATTATAGTAATACATATGAGTGTGCAAG 336
QY 181 AGAATGAAAGGCAAGATTAACGATGAACCCATTACTAGCTTGGCTGTACAGACC 240
Db 337 CGAATATGAAGGCAAGATTAACGATGAACCCATTACTAGCTTGGCTGTACAGACC 396
QY 241 AATACTGAAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGGTGCAAGTGGAGA 300
Db 397 AATACTGAAAGGCAAGTGTGTCAGATGCTTAAGATTAAGAAAGGTGCAAGTGGAGA 456
QY 301 ATCTATATTAATTTGGCTAACTTCTTAACTTATGATTAAGTAAGAAAGCTTACCAT 360
Db 457 ATCTATATTAATTTGGCTAACTTCTTAACTTATGATTAAGTAAGAAAGCTTACCAT 516
QY 361 GCCCATGCCAGCCCTTAATGTCGGGTGACATGATTAAGCACTATGATTAATTTACT 420
Db 517 GCCCATGCCAGCCCTTAATGTCGGGTGACATGATTAAGCACTATGATTAATTTACT 576
QY 421 CTATGTTCTCTCTTTTGAAGTGTGTAAGATGCTTTTGAAGCACTGCAAG 480
Db 577 CTATGTTCTCTCTTTTGAAGTGTGTAAGATGCTTTTGAAGCACTGCAAG 636
QY 481 ATGTTTACTTAATCTAGTGTGCAATGATTAAGTGAAGCTCTAGTGAACGATGCTGT 540
Db 637 ATGTTTACTTAATCTAGTGTGCAATGATTAAGTGAAGCTCTAGTGAACGATGCTGT 696
QY 541 AATCTACTGTACACACTACTGTGTGTGTGCTTAACTCTTAACTATTCACGTGCT 599
Db 697 AATCTACTGTACACACTACTGTGTGTGTGCTTAACTCTTAACTATTCACGTGCT 756
QY 600 TAGTAATACCAATCATTTACACACTGTGTATCATGTGTGAGGCTGC 645
Db 757 TAGTAATACCAATCATTTACACACTGTGTATCATGTGTGAGGCTGC 803

RESULT 3
CG154043 994 bp DNA linear GSS 21-AUG-2003
LOCUS CG154043/c
DEFINITION PUF2S22TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM5BMA0770C19,
LOCUS CG154043 genomic survey sequence.
ACCESSION CG154043
VERSION CG154043.1 GI:34044844
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

|||||
Db 517 ACTGG-ATTGCGCTTGCTGCTACATGCGTGCCTAAATATTGAAAAGGTACATGAGAGAA 575
|||||
Qy 302 TCTATATATTTTGGCTAACTCTT--AGTTACATATGATTGATGAGAAAGCCCTACCAT 360
|||||
Db 576 TCTATATATTTTGGCTAACTCTTCAAAATTTACTATTGATTGAGAAAAGCCCTACCAT 635
|||||
Qy 361 GCCCATCCAGCCCTA---ATGTCCCGGTGACATGATTGAGCCAGTACTATGATTAA 416
|||||
Db 636 GCCATCCAGCATCTTATATGCTGGTGACATGATCGAGCCAGTACTATGATTAA 695
|||||
Qy 417 TACTCTATTTGCTCTCTTTTGTAGTGTGATATAAGATGCTT---TTTGGAGCCAC 472
|||||
Db 696 AACCTATTGTTCTCTTTTGTAGTGTATATAAGATGCTTCTTTTGTGAGCCAC 755
|||||
Qy 473 TCGAGAGATTTACTTAACTCTAGTCCGAATGATGGAGCTGAGTGAACAGCATG 532
|||||
Db 756 ACGAAGAGATTTACTTAACTCTAGTGCACAAATGATTGAAGCTCCCTGTGTACGTTTG 815
|||||
Qy 533 TGCTCTGTAATCTACTG 549
|||||
Db 816 TCATCTCTTATTCATG 832

RESULT 5
CG042359 432 bp DNA linear GSS 19-AUG-2003
LOCUS CG042359
DEFINITION PUIUB5TB ZM 0.6_1.0_KB Zea mays genomic clone ZMMBTA0612P01,
genomic survey sequence.
ACCESSION CG042359
VERSION CG042359.1 GI:33914539
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 432)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennezen,J.
Maize Genomics Consortium
Unpublished (2003)
COMMENT Other GSSs: PUIUB5TD
Contact: Cathy WhiteLaw
TIGR

TITLE 912 Medical Center Drive, Rockville, MD 20850, USA
JOURNAL Tel: 301-838-5843
Other GSSs: PUIUB5TD
Contact: Cathy WhiteLaw
COMMENT Email: whiteLaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
Source
1..432
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0612P01"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Query Match 59.3%; Score 382.4; DB 10; Length 432;
Best Local Similarity 99.5%; Pred. No. 5.4e-90;
Matches 394; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 251 AATGCACTTGCTAGCATGCTTAAGTATTGAAAAGGTACAT-GGAGAAATCTATATT 309
|||||
Db 7 AATGCACTTGCTAGCATGCTTAAGTATTGAAAAGGTACATGGGAGAAATCTATATT 66
|||||
Qy 310 AATTTGGCTAACTCTTATGATTGATTGATGAGAAAAGCTTACCATTTGCCATGCC 369

|||||
Db 67 ATTTGGCTAACTCTTGTGTTACTATTGATTGATGAGAAAGCTTACCATTTGCCATGCC 126
|||||
Qy 370 AGCCCTAAATGTCCTGGGTGACATGATTGAGCCAGTACTATGATTAAATTTCTATTTGTC 429
|||||
Db 127 AGCCCTAAATGTCCTGGGTGACATGATTGAGCCAGTACTATGATTAAATTTCTATTTGTC 186
|||||
Qy 430 TCTTTTGTGAGTCTGTATTAAGATGCTTTTGTGAGCACTCGAAGATGTTTACT 489
|||||
Db 187 TCTTTTGTGAGTCTGTATTAAGATGCTTTTGTGAGCACTCGAAGATGTTTACT 246
|||||
Qy 490 TAACTCTAGTGGCCATGATTGAGCTTCAAGTGCACACGATGCTCTGTATTTACTG 549
|||||
Db 247 TAACTCTAGTGGCCATGATTGAGCTTCAAGTGCACACGATGCTCTGTATTTACTG 306
|||||
Qy 550 TCAACACTCTCTGTGTGTGTGCTTAAACTTAACTTAACTTCAAGTGGCTAGTAATTAC 609
|||||
Db 307 TCACCACTTACCTCTGTGTGTGTGCTTAAACTTAACTTAACTTCAAGTGGCTAGTAATTAC 366
|||||
Qy 610 CAATCATTTTACACACTGTTTACATGTGTAGGGCTGC 645
|||||
Db 367 CAATCATTTTACACACTGTTTACATGTGTAGGGCTGC 402

RESULT 6
CC642785 800 bp DNA linear GSS 19-JUN-2003
LOCUS CC642785/c
DEFINITION OGMDD19TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMA0555C14,
genomic survey sequence.
ACCESSION CC642785
VERSION CC642785.1 GI:32028341
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 800)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteerback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunez,G.A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
COMMENT Other GSSs: OGMDD19TV
Contact: Cathy WhiteLaw
TIGR

TITLE 912 Medical Center Drive, Rockville, MD 20850, USA
JOURNAL Tel: 301-838-5843
Other GSSs: OGMDD19TV
Contact: Cathy WhiteLaw
COMMENT Email: whiteLaw@tigr.org
Seq primer: TR
Class: methylation filtered.

FEATURES
Source
1..800
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0555C14"
/clone_1lb="ZM_0.7_1.5_KB"
/note="Vector: pBSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 40.2%; Score 259; DB 9; Length 800;
Best Local Similarity 97.4%; Pred. No. 2.4e-57;
Matches 295; Conservative 0; Mismatches 5; Indels 3; Gaps 3;
Qy 346 AGAAGGCTTACCAATTG-CCCATGCCAGCCCTAATGTCCCGTGACATGATTGAGCCAGTA 404
|||||
Db 800 AGAAGGCTTACCAATTG-CCCATGCCAGCCCTAATGTCCCGTGACATGATTGAGCCAGTA 741
|||||
Qy 405 CTATGATTAAATTACTTATTTGTT-CTCCTTTTGTAGTGTGTATTAAGATGCTCTTTT 463

Db	740	CTATGATTAATTACTGATTTGCTCTCTTTTGGAGTGTGATAAGATGTCCTTTT	681
Qy	464	TTGAGCCACTGAGAAAGATGTTTACTTAATCTCTAGTGGCGCAATGATTTGAGCTCTCAGTG	523
Db	680	TTGAGCCACTGAGAAAGATGTTTACTTAATCTCTAGTGGCGCAATGATTTGAGCTCTCAGTG	621
Qy	524	CAAGCGATGCTCTGTAATCTACTGTCACACACTA-CCTGTAGTGGTGTCTTAACTCT	582
Db	620	CAAGCGATGCTCTGTAATCTACTGTCACACACTA-CCTGTAGTGGTGTCTTAACTCT	561
Qy	583	AAACTATTCACAGTGGCTAGTAATTCACAAATCATTTACACAAGCTGTTCATGTGTAGGCG	642
Db	560	AAACTATTCACAGTGGCTAGTAATTCACAAATCATTTACACAAGCTGTTCATGTGTAGGCG	501
Qy	643	TGC 645	
Db	500	TGC 498	
RESULT 7			
LOCUS	CG155200	975 bp	DNA
DEFINITION	PUCN04TB ZM 0.6_1.0 KB zea mays genomic clone ZMMBT0788A08,		linear GSS 21-AUG-2003
ACCESSION	CG155200		
VERSION	CG155200.1	GI:34046001	
KEYWORDS	GSS.		
SOURCE	Ze mays		
ORGANISM	Ze mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 975)		
AUTHORS	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Renwick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benneren,J.		
TITLE	Maize Genomics Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Other GSSs: PUCN04TD		
	Contact: Cathy Whitelaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whitelaw@cigr.org		
	Seq primer: TP		
	Class: sheared ends.		
FEATURES	Location/Qualifiers		
Source	1..975		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/strain="B73"		
	/db_xref="taxon:4577"		
	/clone="ZMMBT0788A08"		
	/clone_1lb="ZM_0.6_1.0_KB"		
	/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high		
	COT selected genomic DNA library"		
ORIGIN			
Query Match	35.1%	Score 226.6;	DB 10; Length 975;
Best Local Similarity	97.7%;	Pred. No. 8.9e-49;	
Matches 251; Conservative	0;	Mismatches 4;	Indels 2; Gaps 2;
Qy	1	GTCAAGTTCATTCCTGCTCTCTCTGTTATGTTCTTTTATATTAACAGCGCTGACAAAGCT	60
Db	256	GTCAAGTTCATTCCTGCTCTCTCTGTTATGTTCTTTTATATTAACAGCGCTGACAA-CT	198
Qy	61	ATTAAGCTTGATATGCAATATATATATTAACAAGTTAGTACACAAGTTTGTACTTCAAG	120
Db	197	ATTAAGCTTGATATGCAATATATATTAACAAGTTAGTACACAAGTTTGTACTTCAAG	138
Qy	121	TCTTTAACTATATGTTGGTCGAATTAAGATTATAGTATTCATATGAAGGTGGCAAG	180

Db	137	TCCTTTAACTATAGTGTGGTCAGTAAGATTATGATTAATCCATATAGTAAGGTGTTGCAAG	78
Qy	181	AGAACTAGAAAGCGAAAGATTAACGGATGAACCCATTACTAGCTTTGGCTGTATCAGA-C	239
Db	77	CGAATATGAAAGGCAAAAGATTAACGATGAACCATTACTAGCTTTGGCTGTATCAGACC	18
Qy	240	CAATTAAGCTGGAATGCA	256
Db	17	CAATTAAGCTGGAATGCA	1
RESULT 8			
CC400812/c		734 bp	DNA
LOCUS			linear
DEFINITION	PUGX1.8TD ZM_0.6_1.0_KB	Zea mays genomic clone ZM8Bta249D12,	GSS 19-MAY-2003
ACCESSION	CC400812		
VERSION	CC400812.1	GI:30880902	
KEYWORDS	GSS.		
SOURCE			
ORGANISM	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 734)		
AUTHORS	WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Benmetzen,J.		
TITLE	Maize Genomics Consortium		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Cathy WhiteJaw		
	TIGR		
	9712 Medical Center Drive, Rockville, MD 20850, USA		
	Tel: 301-838-5843		
	Fax: 301-838-0208		
	Email: whiteJaw@cigr.org		
	Seq primer: TP		
	Class: sheared ends.		
FEATURES	Location/Qualifiers		
source	1..734		
	/organism="Zea mays"		
	/mol_type="genomic DNA"		
	/strain="B73"		
	/db_xref="taxon:4577"		
	/clone="ZM8Bta249D12"		
	/clone_1lb="ZM_0.6_1.0_KB"		
	/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high		
	COT selected genomic DNA library"		
ORIGIN			
Query Match	11.9%;	Score 77;	DB 9; Length 734;
Best Local Similarity	63.1%;	Pred. No. 2.8e-09;	
Matches	190;	Conservative 0;	Mismatches 70; Indels 41; Gaps 3;
Qy	280	TAGAAAGGTGATCGATGAGATCTATATTATTTGGCTACTCTTTAGTTACTATTGA	339
Db	551	TAAACCGCACTTGAATATATATGATGATGTTCTGGCTAACCTTCTAGTTACTATTGA	492
Qy	340	TTGATGAGAAAGCCATACATTGGCCATGCGAGCCCTAA-----TGTCCCGG	385
Db	491	TTGATGAGAAATCCATCCGTTTCCATGCGACGACACTACACTACTCTCTGTCTCGG	432
Qy	386	TGACATGATGAGCGACGATCACTATGATTAATTTACTCTAATGTTCTCTTTTGAAGTCT	445
Db	431	TGACATGACGAGCGACGATCACTGATGATTAATGATGTTGCTCTCTTTTGAAGTCT	372
Qy	446	GTATTAAG-----TGTCTTTTGTGAGCACTCGAGA	479
Db	371	ACTCCACAAAGATGTCCTCGGCTCTCTCTCTCTCTCTTTGTGCGACCCACAGAGA	312
Qy	480	GATG-TTACTTAATCTAGTGGCAATGATTTGAGGCTCTGATGCAACGATGTGCTCT	538

Db 311 GATGTTTACTTAAGTGCATGATGAAAGCTCTGTACTAGCGTGCCCT 252
Qy 539 G 539
Db 251 G 251

RESULT 9
CG031509 886 bp DNA 1linear GSS 19-AUG-2003
CG031509/c
LOCUS
DEFINITION
PUFRL237B_ZM_0.6_1.0_KB Zea mays genomic clone ZMMB180656C22,
genomic survey sequence.
ACCESSION
CG031509
VERSION
CG031509.1 GI:33903665
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 886)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Benmetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFRL237D
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source
1..886
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB180656C22"
/note="Vector: PCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN
Query Match 11.7%; Score 75.4; DB 10; Length 886;
Best Local Similarity 62.8%; Pred. No. 7.6e-09;
Matches 189; Conservative 0; Mismatches 71; Indels 41; Gaps 3;

Qy 280 TAGAAAGGTAGATGGAGATATATATTTGGCTAATCTTATGATCTATGA 339
Db 727 TAAACACGACACTTGAATATATGATGATCTGGCTAACCTTCTAGTACTATGA 668
Qy 340 TTGATGAAAGCCTACCATTTGCCATGCCAGCCCTAA-----TGTCCCG 385
Db 667 TTGATGAAATCTTACCGTTTCCATGCCACGACCTACACTCTCGTGTCTG 608
Qy 386 TGACATGATGAGCAGTACTATGATTAATTTACTTATGTTTCTCTTTTGGAGTCT 445
Db 607 TGACATGACGAGCAGTACTATGATTAATTTACTTATGTTTCTCTTTTGGAGTCT 548
Qy 446 GTATPAGA-----TGTCTTTTGGAGCAGTCCGAGAA 479
Db 547 ACTCCAGAAATGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 488
Qy 480 GATG-TTACTTAAGTGCAGAAATGATGAGCTCTCAGTCAACGATGTGCTCT 538
Db 487 AATGTTTACTTAAGTGCAGAAATGATGAGCTCTCTCTCTCTCTCTCTCTCTCT 428
Qy 539 G 539

Db 427 G 427

RESULT 10
CG031059 858 bp DNA 1linear GSS 26-AUG-2003
CG031059/c
LOCUS
DEFINITION
OG5CY437C_ZM_0.7_1.5_KB Zea mays genomic clone ZMMB180834G13,
genomic survey sequence.
ACCESSION
CG031059
VERSION
CG031059.1 GI:34228219
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 858)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Maize Genomics Consortium
Unpublished (2002)
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.

FEATURES
Location/Qualifiers
source
1..858
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMB180834G13"
/note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 11.4%; Score 73.6; DB 10; Length 858;
Best Local Similarity 64.3%; Pred. No. 2.3e-08;
Matches 180; Conservative 0; Mismatches 59; Indels 41; Gaps 3;

Qy 301 ATCTATATATTTTGGCTAATCTTACTTACTATGATGAAAGCCTACCAT 360
Db 5 ATATGAAATGTTGGCTAACCTTCTCTAGTACTATGATGAAATCTTACCGTT 64
Qy 361 GCCATGCCAGCCCTAA-----TGTCCCGTGAATGATGAGCCAGTACT 406
Db 65 TCCATGCCACGACCTACACTCTCTGTCTCTGTGATGACGACGACAGTACA 124
Qy 407 ATGATTAATTTACTTATGTTCTCTCTTTTGAAGTGTATPAGA----- 453
Db 125 CTGACTGATTAATGATGTTGCTCTCTTTTGAAGTGTACTCCAAAGATGCTCGGC 184
Qy 454 -----TGTCTTTTGAAGCAGTCCGAGAGAGT-TTTACTTAATCTAGT 499
Db 185 CTCTCTCTCTCTCTCTTTTGAAGCAGTCCGAGAGATTTTACTTAATCTAGT 244
Qy 500 GCGCAATGATGAGCTCTCAGTCAACGATGTGCTCTG 539
Db 245 GCACATGATGAAAGCTCTCTGTACTAGGCTGTGCTG 284

RESULT 11
CC721634 345 bp DNA 1linear GSS 19-JUN-2003
CC721634/c
LOCUS
DEFINITION
OG2AD277H_ZM_0.7_1.5_KB Zea mays genomic clone ZMMB180741F06,
genomic survey sequence.
ACCESSION
CC721634

VERSION	GC712634.1	GI:33126410
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS	1 (bases 1 to 345)	
TITLE	WhiteLw.C.A., Quackenbush, J., Van Aken, S., Utterback, T., Reenick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numborg, A., Robbins, D. and Lakey, N.	
JOURNAL	Consortium for Maize Genomics	
COMMENT	Unpublished (2002)	
	Other_GSS: OG2AD27TV	
	Contact: Cathy WhiteLw	
	TIGR	
	9712 Medical Center Drive, Rockville, MD 20850, USA	
	Tel: 301-838-5843	
	Fax: 301-838-0208	
	Email: whiteLw@tigr.org	
	Seq primer: TK	
	Class: methylation filtered.	
FEATURES	Location/Qualifiers	
SOURCE	1..345	
	/organism="Zea mays"	
	/mol_type="genomic DNA"	
	/strain="B73"	
	/db_xref="taxon:4577"	
	/clone="ZMIBM0741F06"	
	/clone_1lb="ZM_0.7.1.5_KB"	
	/note="Vector: pBCSK-; Site 1: HincII. 0.7-1.5 kb methylation filtered genomic DNA library"	
ORIGIN		
Query Match	7.7%: Score 49.8; DB 9; Length 345;	
Best Local Similarity	71.0%: Pred. No. 0.038; 27; Indels 0; Gaps 0;	
Matches	66; Conservative 0; Mismatches 27; Indels 0; Gaps 0;	
Oy	280 TAGAAGGTAGCATGAGATCATATTTATTTGGCTTAACCTTCTTACTTACTTATGA 339	
Db	246 TAAACCGACGACCTGAAATATATGAAATGTTCTGCGTACCTTCTAGTTACTTATGA 305	
Oy	340 TTGATGAGAAAGCTTACCATTTGCCATGCCAGC 372	
Db	306 TTGATGAGAAATCCATCCGTTCCCATGCCAGC 338	
RESULT 12		
DN487904/c		
LOCUS	DN487904 597 bp mRNA linear EST 10-MAR-2005	
DEFINITION	R014B11.3R Populus root cDNA library Populus tremula x Populus tremuloides cDNA clone R014B11.3', mRNA sequence.	
VERSION	DN487904	
KEYWORDS	DN487904.1 GI:60697634	
SOURCE	EST.	
ORGANISM	Populus tremula x Populus tremuloides	
	Populus tremula x Populus tremuloides	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid I; Malpighiales; Salicaceae; Salicaceae; Populus.	
REFERENCE	1 (bases 1 to 597)	
AUTHORS	Sterky, P., Bhalerao, R.R., Unnberg, P., Segerman, B., Nilsson, P., Brunner, A.M., Charbonnel-Campaa, L., Lindvall, U.J., Tander, K., Struhs, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P., Nilsson, O., Sandberg, G., Karlsson, J., Lundberg, J. and Jansson, S.	
	A Populus EST resource for plant functional genomics	
	Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)	
TITLE	Other ESTs: R014B11, R014B11.5PR	
JOURNAL	Contact: Bo Segerman	
PUBMED	Umea Plant Science Center, Department of Plant Physiology	
COMMENT	Umea University	
	901 87 Umea, Sweden	

	Tel: +46 90 786 5279
	Fax: +46 90 786 6676
	Email: bo.segerman@plantphys.umu.se.
FEATURES	Location/Qualifiers
SOURCE	1..597
	/organism="Populus tremula x Populus tremuloides"
	/mol_type="mRNA"
	/db_xref="taxon:47664"
	/clone="R014B11"
	/issue_type="root"
	/clone_lib="Populus root cDNA library"
ORIGIN	
Query Match	7.4%; Score 47.6; DB 8; Length 597;
Best Local Similarity	51.1%; Pred. No. 0.16;
Matches 137; Conservative	0; Mismatches 129; Indels 2; Gaps 1;
OY	55 AAAGCTAAAGCTGATGACGTGAATTAATAACAAGT--TAGCTACACAATTGGT 112
DB	366
	425 AAAGCTAAAGCTGATGACGTGAATTAATAACAAGT--TAGCTACACAATTGGT 366
OY	113 ACTCAAGCTCTTTAAGCTATATGTTGGTCAGATAGAATTAGACTAATCCATAGAAGT 172
DB	306
	365 AAAAAAATTTATTCATATTTGATGTGATAGATTAGAAAAGAAAAAATTCATTTAAAGAA 306
OY	173 GTTGCAAGAGAACATGAAAGCAGAAAGATTAACCGATGAACCATTAAGCTTTGGCTGT 232
DB	246
	305 TTACCCTTAACCACTTAACCAAGATTAATTAATAAAAGATCCGATACCTGTGCATTT 246
OY	233 ATCAGACCAATTAATTTGAATGCACTTGCTGTACGACGCCATAGATTATGAAAAAGTAGC 292
DB	186
	245 TCAAGATCAAAAAAATAAAATTTCCACGTAAGCAAGATTTATGTTTTTTTAAAGAGTC 186
OY	293 ATGGAGAAATCTATATTTATTTTGGCTAA 320
DB	158
	185 TAGACATTAATAATGATGAAGATTA 158
RESULT 13	
CL180658/c	754 bp DNA linear GSS 06-JAN-2004
LOCUS	104_330_10896176_116_31930_330 Sorghum methylation-filtered library
DEFINITION	(L1BID: 104) Sorghum bicolor genomic clone 10896176, genomic survey sequence.
ACCESSION	CL180658
VERSION	CL180658.1 GI:40693181
KEYWORDS	GSS.
SOURCE	Sorghum bicolor (sorghum)
ORGANISM	Sorghum bicolor
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.
AUTHORS	1 (bases 1 to 754) Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,B., Rohlfing,T., Fries,J., Bradford,K., McNamee,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korf,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeldoh,J.A. and Mattingsen,R.A.
TITLE	Sorghum genome sequencing by methylation filtration
JOURNAL	PLoS Biol. 3 (1), e13 (2005)
PUBMED	15660154
COMMENT	Contact: Bedell JA Orion Genomics, LLC 4061 Forest Park Ave, St. Louis, MO 63108, USA Tel: 314 615 6979 Fax: 314 615 6975 Email: jbedell@oriongenomics.com Plate: 390 row: n column: 08 Seq primer: T3 Reverse Clase: methylation filtered High quality sequence stop: 754. Location/Qualifiers 1..754
FEATURES	
SOURCE	1..754

```

/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="RTx623"
/db_xref="taxon:4558"
/clone_1lb="10896176"
/clone_1lb="Sorghum methylation-filtered library (LabID:
104)"
/notes="Organ: leaf; Vector: pBCKS(-); Site 1: HindIII; DNA
prepared from purified nuclei was randomly sheared,
end-repaired, size fractionated to enrich for the 0.5 to 5
kb fraction, ligated into HindIII-digested pBCKS(-) vector
and electroporated into E. coli cells. This is a
methylation-filtered library."

```

ORIGIN

```

Query Match      6.6%; Score 42.8; DB 10; Length 754;
Best Local Similarity 48.1%; Pred. No. 3;
Matches 151; Conservative 0; Mismatches 162; Indels 1; Gaps 1;

QY 99 TACCAAGTTTGTACTTCAAGTCTTTTAACTATATGTGTCATTAAGATTATAGTA 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 507 TATCTTAATATATGTCATTCATTCATTAATGCTCTTTTAAAGTTATAGATCTTACTA 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 159 ATCCATATGAAGGTGTTGCAAGAACATGAAAGGCAAGATA-AACGATGAACCCATT 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 TTTTAATAATATATAGATGACCAACAGATATTAAGTATAGAAAAAACAACAGAT 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 218 ACTAGCTTGGCTGTATCAAGCAATCACTGTCATGTCATGCTTATGCTTATGCT 277
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 387 TCCAAATTAACAAATTAAGAACAAATTTAGAAAAAAATGATTAATGCTTCATATATA 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 278 ATTAGAAAGGTAGCATGAGAGATCTATATATTTTGGCTAACTTTAGTACTATT 337
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 327 TTTTATGATTTAAATTAATTAATTAATTTTGAATCAAGCTTAATTTTATCT 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 338 GATTGATGAGAAAGCTTACCATGCGCAGCCCTTAATGTCGCGTACATGATGA 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 267 TTTTGAATAAATAAACAATTAACAACAGCCACATGTCATTAATTAATTC 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 398 GCCAGTCTATGAT 411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 207 GACAGTTTAAAGT 194
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 14
BP526721/c      375 bp      mRNA      linear      EST 05-NOV-2004
LOCUS          BP526721 MAT001 Nicotiana tabacum cDNA clone BY11463, mRNA
DEFINITION
sequence.
ACCESSION      BP526721
VERSION        BP526721.1 GI:52830448
KEYWORDS
SOURCE
ORGANISM      Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 375)
Matsunaka,K., Demura,T., Galis,I., Horiguchi,T., Sasaki,M.,
Tashiro,G. and Fukuda,H.
A Comprehensive Gene Expression Analysis Toward the Understanding
of Growth and Differentiation of Tobacco BY-2 Cells
Plant Cell Physiol. 45 (9), 1280-1289 (2004)
15509851
Contact: Ken Matsunaka
Morphogenesis Research Group
RIKEN Plant Science Center
1-7-2 Sushirocho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9575
Fax: 81-45-503-9573
Email: by2@psc.riken.go.jp, URL:http://mrg.psc.riken.go.jp/btrc/
The cDNA library was constructed from mRNA isolated from lag (9 h),
log (72 h) and stationary (7 days) old BY-2 cells.

```

```

FEATURES
source
Seq primer: M13 forward.
Location/Qualifiers
1..375
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/cultivar="Bright Yellow No.2"
/db_xref="taxon:4097"
/clone_1lb="BY11463"
/cell_line="BY-2"
/clone_1lb="MAT001"
/notes="Vector: pGEM-T easy; primer: M13 forward; mRNA
obtained from lag, log and stationary phase cells"

```

ORIGIN

```

Query Match      6.5%; Score 41.8; DB 3; Length 375;
Best Local Similarity 53.3%; Pred. No. 5;
Matches 88; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 89 ACAAGTTAGCTACCAAGTTTGTACTTCAAGTCTTTTAACTATATGTTGTCATTAAG 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 370 ACAAGTTAGCTGATGATTTGTGTCACAAAGATGATATTTCTTACATGATCAATTAAT 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 149 ATTATAGATTAATCAATATGAAGTGTTCACAGAACATGAAGCAAAAGATTAACGAT 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 310 AATTAGTATTCATGTTCAAGGTGAGGAAACACAAAAGAACGAGAAATTAAGCA 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 209 GAACCATTAATCTAGCTTTGGCTGTATCAAGCAATTAATTAAT 253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 AGAGCAATTAATCTCAACATCTCTTCAGGCTCTCAAGTTGAAT 206
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 15
CC950911      684 bp      DNA      linear      GSS 18-AUG-2003
LOCUS          BO1BR08TF_BO_1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION
BO1BR08, genomic survey sequence.
ACCESSION      CC950911
VERSION        CC950911.1 GI:33788146
KEYWORDS
SOURCE
ORGANISM      Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 684)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Mortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)
15805490
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..684
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="NO1000DH3"
/db_xref="taxon:3712"
/clone_1lb="BO1BR08"
/clone_1lb="BO_1.4.1.6_KB_nuc"
/notes="Vector: pHO52; Site 1: BclXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHO52 using BclXI linkers"

```

```

FEATURES
source

```

```

ORIGIN
Query Match      6.5%; Score 41.8; DB 9; Length 684;

```

Best Local Similarity 50.2%; Pred. No. 5.5;
 Matches 103; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy	386	TGACATGATTGAGCCAGTACTATGATTAAATTACTTATTGTTCTCCTTTTGGAGTGT	445
Db	138	TGACATCAATCTGCGATTACTCGGTTATTTCTATCTGGGTTTCTCCCTCGTTTCAC	197
Qy	446	GTAATAAGATGTCCTTTTGGAGCCACTCGAAGATGTTTACTTACTAGTGGCAA	505
Db	198	GTTGAAGCAGAGCTCGTGAATGCCCCCAGAGTCTATCCTTGAAACTTCCCTCAGCAA	257
Qy	506	TGATTGAGCTCTCAGTCAAGCATGCTGTGAATCTACTGTCAACCACTACTGTGA	565
Db	258	GGATTAGATCTCTTAACATCATTTGAATTGAGCTTTGAGTACCCAGAAATTACTAACG	317
Qy	566	GTTGTGCTTAAACTTAACATAAT	590
Db	318	CTGCCCCATTTGGCTCCCACTAAT	342

Search completed: February 12, 2006, 00:46:32
 Job time : 3707 secs

THIS PAGE BLANK (USPTO)

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

THIS PAGE BLANK (upto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 12, 2006, 00:06:08 ; Search time 403 Seconds
(without alignments)
1439.108 Million cell updates/sec

Title: US-10-759-602-1_COPY_4420_5064

Perfect score: 645
Sequence: 1 GTCAGGTCAATTCGCTT.....TGTACATGTAGGCTGC 645

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA New:
1: /cgn2_6/ptcdatara/1/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/ptcdatara/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptcdatara/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptcdatara/1/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/ptcdatara/1/pubpna/US09_NEW_PUB.seq:*
6: /cgn2_6/ptcdatara/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptcdatara/1/pubpna/US11_NEW_PUB.seq1:*
8: /cgn2_6/ptcdatara/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptcdatara/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptcdatara/1/pubpna/US11_NEW_PUB.seq4:*
11: /cgn2_6/ptcdatara/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptcdatara/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	39.2	6.1	5052	9 US-11-112-944-2	Sequence 2, Appl1
C 12	38.8	6.0	3222	11 US-11-098-686-9068	Sequence 9068, Ap
C 13	38.8	6.0	1457619	11 US-11-098-686-8739	Sequence 8739, Ap
C 4	38.4	6.0	166442	11 US-11-121-086-104	Sequence 104, Appl
C 5	37.2	5.8	1844	7 US-10-623-155-88	Sequence 88, Appl
C 6	36.4	5.6	46215	7 US-10-995-561-13463	Sequence 13463, A
C 7	36.2	5.6	61187	11 US-11-117-187-209	Sequence 209, Appl
C 8	34.8	5.4	566	11 US-11-136-527-941	Sequence 941, Appl
C 9	34.8	5.4	2526	11 US-11-136-527-5037	Sequence 5037, Ap
C 10	34.8	5.4	162173	6 US-10-903-375-34	Sequence 34, Appl1
C 11	34.6	5.4	162173	11 US-11-121-086-72	Sequence 72, Appl1
C 12	34.6	5.3	601	7 US-10-750-185-29889	Sequence 29889, A
C 13	34.2	5.3	601	7 US-10-750-623-29889	Sequence 29889, A
C 14	34.2	5.3	3232	7 US-10-750-185-62480	Sequence 62480, A
C 15	34.2	5.3	3232	7 US-10-750-623-62480	Sequence 62480, A
C 16	34.2	5.3	5003	7 US-10-995-561-391	Sequence 391, Appl
C 17	34.2	5.3	61718	7 US-10-995-561-13326	Sequence 13326, A
C 18	34.2	5.3	1201	7 US-10-750-185-61404	Sequence 61404, A
C 19	34	5.3	1201	7 US-10-750-623-61404	Sequence 61404, A
C 20	34	5.3	19940	7 US-10-829-826B-19	Sequence 19, Appl
C 21	34	5.3	19940	7 US-10-829-826B-19	Sequence 19, Appl

C 22	34	5.3	27528	7 US-10-829-826B-20	Sequence 20, Appl
C 23	33.6	5.2	1074	7 US-10-750-185-51378	Sequence 51378, A
C 24	33.6	5.2	1074	7 US-10-750-623-51378	Sequence 51378, A
C 25	33.6	5.2	5244	7 US-10-750-185-26190	Sequence 26190, A
C 26	33.6	5.2	5244	7 US-10-750-623-26190	Sequence 26190, A
C 27	33.4	5.2	1644	7 US-10-750-185-40610	Sequence 40610, A
C 28	33.4	5.2	1644	7 US-10-750-623-40610	Sequence 40610, A
C 29	33.4	5.2	100008	11 US-11-124-367A-5058	Sequence 5058, Ap
C 30	33.2	5.1	897	7 US-10-750-185-30270	Sequence 30270, A
C 31	33.2	5.1	897	7 US-10-750-623-30270	Sequence 30270, A
C 32	33.2	5.1	992	11 US-11-136-527-1674	Sequence 1674, Ap
C 33	33.2	5.1	992	11 US-11-136-527-5770	Sequence 5770, Ap
C 34	33.2	5.1	1268	7 US-10-750-185-33787	Sequence 33787, A
C 35	33.2	5.1	1268	7 US-10-750-623-33787	Sequence 33787, A
C 36	33.2	5.1	162173	11 US-11-121-086-72	Sequence 72, Appl1
C 37	33.2	5.1	168753	11 US-11-181-234-1	Sequence 1, Appl1
C 38	33	5.1	754	7 US-10-750-185-42665	Sequence 42665, A
C 39	33	5.1	754	7 US-10-750-623-42665	Sequence 42665, A
C 40	33	5.1	1299	7 US-10-750-185-27962	Sequence 27962, A
C 41	33	5.1	1299	7 US-10-750-623-27962	Sequence 27962, A
C 42	33	5.1	1420	7 US-10-750-185-45147	Sequence 45147, A
C 43	33	5.1	1420	7 US-10-750-623-45147	Sequence 45147, A
C 44	33	5.1	1082144	11 US-11-117-187-211	Sequence 211, Appl
C 45	33	5.1	1125000	7 US-10-995-561-13286	Sequence 13286, A

ALIGNMENTS

RESULT 1
US-11-112-944-2/c
; Sequence 2, Appl1cation US/11112944
; Publication No. US2005024872A1
; GENERAL INFORMATION:
; APPLICANT: Hartig, Cole
; TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers
; FILE REFERENCE: 05-325-US
; CURRENT APPLICATION NUMBER: US/11/112,944
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,757
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 5052
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-944-2

Query Match 6.1%; Score 39.2; DB 9; Length 5052;
Best Local Similarity 48.6%; Pred. No. 0.57;
Matches 107; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY	271	CTTAAGTATTAGAAAGTACGAGGAGATCATATTTTGGCTAATCTTTAGT	330
DB	1694	CTTAAGTATTAGAAAGTACGAGGAGATCATATTTTGGCTAATCTTTAGT	1635
QY	331	TACTATTGATGATGAGAAAGCTTACCATTCGCCATCCAGCCCTAATGTCGGTGACA	390
DB	1634	CTGATATTAAATTTAGTTGAGTTCTTAAGATCAAGGATGATGATTTGATGATGATG	1575
QY	391	TGATTTGAGGACGATGATGATTTAATTTATCTTATGTTCCCTTTTGGTGGCTGATA	450
DB	1574	TTGTTGTTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1515
QY	451	AGATGTCCTTTTGGTGGCTGACGAGGAGATGTTACTT	490
DB	1514	AGCAACCCCAATTAATCTTATCTTCAAGACGGAATTAATT	1475

RESULT 2
US-11-098-686-9068/c
; Sequence 9068, Appl1cation US/11098686

```
/ Publication No. US20060024696A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ PRIOR FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9068
/ LENGTH: 3222
/ TYPE: DNA
/ ORGANISM: Lawsonia intracellularis
US-11-098-686-9068

Query Match          6.0%; Score 38.8; DB 11; Length 3222;
Best Local Similarity 43.9%; Pred. No. 0.65;
Matches 166; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 98 CTACACAAGTTTGTACTTCAAGTCTTTTAACTATATGTGTGCAATTAAGATTATAGT 157
DB 482 CCAAGGAAGAAAGCGACATTAATGTCTGTAGGTTCAAGGTAAACCTTAATAATAGTTAA 423
QY 158 AATCCATATGAAGGTGTGCAAGAAACATGAAGGCAAGATTAAGCATGAACCAT 217
DB 422 TGAAGTCTTACTTCTGTGTCAAGAAAGTGAAGAAATTCGAAAACTTTGACGGCAT 363
QY 218 ACTAGCTTGTGCTGTATCAGACCAATTAAGTGAATGCACTTGCTAGCATGCGTAAGT 277
DB 362 TCATATATATGTTTATATAGGTTCTTCAACAAAGATCTGTGATTATATCAAGATCATTA 303
QY 278 ATTAGAAAAGGTAGCATGGAGAACTATATATTTTGGCTACTTCTTTAGTTACTATT 337
DB 302 AGTTTATAGTACTAGTGAAGCAATATGTTTACATACGCCCAATTAATGCTTTCATGACAGT 243
QY 338 GATTGATGAGAAAGCCATCACTTCCATGCGACGCCCTTAATGTCGGTGACATGATGA 397
DB 242 CATGTATGAGAAACACGTGATCTTCAATATAAATAAATAGTGTGAGAAATGTTTGA 183
QY 398 GCCAGTACTATGATTAATTAATCTATGTTCTCTTTTGAAGTGTGATTAAGATGTC 457
DB 182 AATCTCTTCTTGTACAAATCTGTCTATATATCAAAATATCATGTTCTTTACGAATGTA 123
QY 458 CTTTTTTGAGCCACTCG 475
DB 122 AGTTTGTGACACCATTG 105

RESULT 3
US-11-098-686-8739
/ Sequence 8739, Application US/11098686
/ Publication No. US20060024696A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ PRIOR FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8739
/ LENGTH: 1457619
/ TYPE: DNA
```

```
/ ORGANISM: Lawsonia intracellularis
US-11-098-686-8739

Query Match          6.0%; Score 38.8; DB 11; Length 1457619;
Best Local Similarity 43.9%; Pred. No. 2.3;
Matches 166; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

QY 98 CTACACAAGTTTGTACTTCAAGTCTTTTAACTATATGTGTGCAATTAAGATTATAGT 157
DB 210262 CCAAGGAAGAAAGCGACATTAATGTCTGTAGGTTCAAGGTAAACCTTAATAATAGTTAA 210321
QY 158 AATCCATATGAAGGTGTGCAAGAAACATGAAGGCAAGATTAAGCATGAACCAT 217
DB 210322 TGAAGTCTTACTTCTGTGTCAAGAAAGTGAAGAAATTCGAAAACTTTGACGGCAT 210381
QY 218 ACTAGCTTGTGCTGTATCAGACCAATTAAGTGAATGCACTTGCTAGCATGCGTAAGT 277
DB 210382 TCATATATATGTTTATATAGGTTCTTCAACAAAGATCTGTGATTATATCAAGATCATTA 210441
QY 278 ATTAGAAAAGGTAGCATGGAGAACTATATATTTTGGCTACTTCTTTAGTTACTATT 337
DB 210442 AGTTTATAGTACTAGTGAAGCAATATGTTTACATACGCCCAATTAATGCTTTCATGACAGT 210501
QY 338 GATTGATGAGAAAGCCATCACTTCCATGCGACGCCCTTAATGTCGGTGACATGATGA 397
DB 210502 CATGTATGAGAAACACGTGATCTTCAATATAAATAAATAGTGTGAGAAATGTTTGA 210561
QY 398 GCCAGTACTATGATTAATTAATCTATGTTCTCTTTTGAAGTGTGATTAAGATGTC 457
DB 210562 AATCTCTTCTTGTACAAATCTGTCTATATATCAAAATATCATGTTCTTTACGAATGTA 210621
QY 458 CTTTTTTGAGCCACTCG 475
DB 210622 AGTTTGTGACACCATTG 210639

RESULT 4
US-11-121-086-104
/ Sequence 104, Application US/11121086
/ Publication No. US20050266459A1
/ GENERAL INFORMATION:
/ APPLICANT: POULSEN, TIM S.
/ TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
/ FILE REFERENCE: 09138.6000-00000
/ CURRENT APPLICATION NUMBER: US/11/121,086
/ PRIOR FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: 60/567,570
/ PRIOR FILING DATE: 2004-05-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 104
/ LENGTH: 186442
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-121-086-104

Query Match          6.0%; Score 38.4; DB 11; Length 186442;
Best Local Similarity 52.5%; Pred. No. 2.3;
Matches 84; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 260 GTGCTGACATGCTTAAGTATTAAGAAAGGTAGCATGGAGAACTATATATTTTGGCTTA 319
DB 133505 GTGTACTATGCCCCATTTAAACAGATTAAGAAATCAGAACGACAGTGAATTAAGTTATTA 133564
QY 320 ACTTCTTATGTTACTATATGATGATGAGAAAGCTTCAACTTGCCATGCGACGCCCTTAAG 379
DB 133565 TGTGTTCTGTGTACTCTGCTGCAAAATTAACACCCCAATCTTAAGAACTATGATTA 133624
QY 380 TCCCGGTGACATGATTAAGCCGACTATATGATTAATTTAC 419
DB 133625 TGCTCATGTATTAATATGAGTCAGAAAGTTTGAACATGTC 133664
```


RESULT 5
US-10-623-155-88/C
Sequence 88, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Peckham, David W.
APPLICANT: Reiter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 88
LENGTH: 1844
TYPE: DNA
ORGANISM: Homo sapiens
US-10-623-155-88

Query Match 5.8%; Score 37.2; DB 7; Length 1844;
Best Local Similarity 47.8%; Pred. No. 1.5;
Matches 108; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 8 TTCATTCTGCTTCTCTGTTTATGTTTATATATACATGCTGACAAAGCTATAAGC 67
DB 1599 TTTAATTTCAATTTCTCTCTTATATTAACCTTTATATAGCATGTTTCCACTACAGT 1540
QY 68 TTGATCTGACATATATATATATACAGTACTACACAAAGTTTGTACTTCAAGCTTTA 127
DB 1539 TTAACATATGACGAAATTTCCCATTTACAGGTAAATGGGTTTAAAGCGCAAGTTAAA 1480
QY 128 ACTAATGTTGTCATATAGATTATGATATCATATGATAGAGTGTTCGAAGAACAT 187
DB 1479 ATGCTTTGAGATTCCTGAATACACCTTTGAACCTTCAATAGAGTTATGTTTAATTT 1420
QY 188 GAAAGCAAAATMAACGATGAACCATTAAGTTAGCTTTGGCTGTA 233
DB 1419 AACCTCATGATAGAGAGGACAGTAGTGCATGCTCTTA 1374

RESULT 6
US-10-995-561-13483
Sequence 13483, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: C1001559
CURRENT APPLICATION NUMBER: US/10/995.561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13483
LENGTH: 46215
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(46215)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13483

Query Match 5.6%; Score 36.4; DB 7; Length 46215;
Best Local Similarity 52.7%; Pred. No. 5.5;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 323 TCTTAGTACTATGATGAGAAAGCTACATGGCCATGACGCCCTAATGTC 382

DB 27870 TCTTTGTGAATTCGAAATGAGAAAAATATTTTTTGCATTTTACCACATCTTA 27929
QY 383 CGGTACATGATGAGCAGTACTATGATTAATTAATCTATTTGCTCTTTTGAGT 442
DB 27930 CCATTTCTGTGTTCTTCACTACTAGTCTCCATCTGAGTGGCTTTTCTTCTT 27989
QY 443 GCTGTATAGATGCTCTTTTGGAGCCAC 472
DB 27990 TTCTTTTCTTTTCTTTTCTTTTGGAGCAC 28019

RESULT 7
US-11-117-187-209
Sequence 209, Application US/11117187
Publication No. US2005026560A1
GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COHENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:308US
CURRENT APPLICATION NUMBER: US/11/117.187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531.120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 611587
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-11-117-187-209

Query Match 5.6%; Score 36.2; DB 11; Length 611587;
Best Local Similarity 54.0%; Pred. No. 12;
Matches 74; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 82 TAAATTAACAAGTTAGCTACACAAGTTTGTACTTCAAGTCTTTTAATTAATGTTGG 141
DB 28263 TTAATTTAGGTTAAAGTTCTAAAGTTATATATATATATATATATATATTTTG 28322
QY 142 CATTAAGTTATGATATTCATATGAGGTGTTCGAAGAACATGAAGCAAGATA 201
DB 28323 GTAAAGATTAAAGTTTATACATTTAGTTTAAACAGATTACAAAGATTACAAAG 28382
QY 202 AACGATGAACCATTA 218
DB 28383 AACGATTAAGCATTA 28399

RESULT 8
US-11-136-527-941/C
Sequence 941, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031696-04100 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136.527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574.294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 941
LENGTH: 566
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-941

Query Match 5.4%; Score 34.8; DB 11; Length 566;
Best Local Similarity 57.7%; Pred. No. 5;
Matches 60; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 397 AGCCAGTACTATGATTAACTTCTATTTCTCTCTTTTGGAGTCTGTATTAAGATGT 456
DB 153 AGCCGCTACTATGATGAATCCGCCCTACTCTTAATTTGCTGAATGAAGMAAAAAAAT 94

QY 457 CTTTTTTTGGAGCACTCGAAGATGTTTACTTAAGTATG 500
DB 93 CTTTATTGTGATTTTTCAGAGACATTTGCTCTAGATGTG 50

RESULT 9
US-11-136-527-5037
; Sequence 5037, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5037
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5037

Query Match 5.4%; Score 34.8; DB 11; Length 566;
Best Local Similarity 57.7%; Pred. No. 5;
Matches 60; Conservative 1; Mismatches 43; Indels 0; Gaps 0;

QY 397 AGCCAGTACTATGATTAACTTCTATTTCTCTCTTTTGGAGTCTGTATTAAGATGT 456
DB 414 AGCCGCTACTATGATGAATCCGCCCTACTCTTAATTTGCTGAATGAAGMAAAAAAAT 473

QY 457 CTTTTTTTGGAGCACTCGAAGATGTTTACTTAAGTATG 500
DB 474 CTTTATTGTGATTTTTCAGAGACATTTGCTCTAGATGTG 517

RESULT 10
US-10-903-375-34
; Sequence 34, Application US/10903375
; Publication No. US20060024794A1
; GENERAL INFORMATION:
; APPLICANT: LI, Shengwen
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Novel Methods for Production of D1-Chain Botulinum Toxin
; FILE REFERENCE: ALLE0012-100 (ROI2003-147)
; CURRENT APPLICATION NUMBER: US/10/903,375
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 2526
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleic acid sequence of HC
US-10-903-375-34

Query Match 5.4%; Score 34.8; DB 6; Length 2526;
Best Local Similarity 47.3%; Pred. No. 7.2;
Matches 105; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 84 ATATTAACAAGTTAGCTACACAAAGTTTGTACTTCAAGTCTTTTAACATAATGTTGTGCA 143

DB 1904 ATTAATATATCTTTTAAATAGCTTCAATATACAAATGATAGTAAAGATTATTTGGGAA 1963

QY 144 ATTAAGTTATGATATCCATATGAAAGTGTGCAAGAACTGAAGCAAGATTAAT 203

DB 1964 ATGATCTTGATATTAATTAAGATTAATTAATGATTAATGATTAATGATTAAT 2023

QY 204 CGATGAACCCATTACTAGCTTGTGCTGTATCAGACCAATTAAGTAAATGACTGTGC 263

DB 2024 TGTATCAATATGATACAAATGATTTTAATACAGAAAGAAATTAATGATTTTAATG 2083

QY 264 TAGATGCTTATGATTAAGAAAGTACATGGAGAAATCTA 305

DB 2084 AAGATATTAATAATTAATTAATAAGATTAAGAAATACAA 2125

RESULT 11
US-11-121-086-72
; Sequence 72, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138,6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 72
; LENGTH: 162173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-72

Query Match 5.4%; Score 34.8; DB 11; Length 162173;
Best Local Similarity 54.8%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 520 AGTCAACGATGCTCTGTATCTATCTACCACTACTCTGTAGTGTGCTTAAAC 579

DB 132077 ACTTGAAGCCAGGTGTTCTTGATGCACTGGCACCTGACCTCAGCCCTGGCAACAGA 132136

QY 580 TCTAACTATTTCCAGCGGTAGTAATTAACATCTTTCACACACTGTACATGTGTAG 639

DB 132137 GCAGACTCTGTCTCAAGAAAAAAGAAAGAAAGAAACATGCAATTTTCCAGAGAG 132196

QY 640 GGCTGC 645

DB 132197 AGCAGC 132202

RESULT 12
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretearsdotter, Solveig
; APPLICANT: Thoreleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345,2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18

```

1 PRIOR APPLICATION NUMBER: 10/650,120
2 PRIOR FILING DATE: 2003-08-27
3 PRIOR APPLICATION NUMBER: 10/067,514
4 PRIOR FILING DATE: 2002-02-04
5 PRIOR APPLICATION NUMBER: 09/811,352
6 PRIOR FILING DATE: 2001-03-19
7 NUMBER OF SEQ ID NOS: 102
8 SOFTWARE: Fastseq for Windows Version 4.0
9 SEQ ID NO: 1
10 LENGTH: 1691140
11 TYPE: DNA
12 ORGANISM: Homo sapiens
13 FEATURE:
14 NAME/KEY: misc feature
15 LOCATION: (1)..(1691140)
16 OTHER INFORMATION: n=a,T,C or G
17 JS-11-091-018-1

```

Query Match	5.4%	Score	34.6	DB	11	Length	169140
Best Local Similarity	52.4%	Pred	No. 39				
Matches	76	Conservative	0	Mismatches	69	Indels	0
						Gaps	0

Qy	8	TTCAATTCGCTCTCTGTATCTCTTATATTAACAGCTCGAAGAAGCATATAAGC	67
Db	1102792	TTTAAATTCGCTCTCTCAGATATTTAATTAATAAGCTGCTGTAGCAAGGGCTTTC	1102793

Db	Seq	Start	End	Score	E-value
0y	68 TTGATACGCAAGTAAATATATACAGTTGTGTACACAGTTTGTACTTCAAGTCCTTTA	127			
1102732	ATAATTTTATGTCAACATTTCTGAGTCACTACTCTGATTTGTTTAAATTCAAATGC	1102673			

Qy	128	ACTATATGTTGGTCATTAAGATTA	152
Db	1102672	AAGATATTGGCTAACATACAATCA	1102648

```

RESULT 13
US-10-750-185-29889/C
Sequence 29889, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29889
LENGTH: 601
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-29889 19866881745929

```

	Query Match	Similarity	Score	DB	Length
Beet	Local	5.3%	34.2	7	601
Matches	87	Conservative	49.7%	Pred. No.	7.3
			0	Mismatches	88
				Indels	0
				Gaps	0

Oy	235	CAGACCAATTA	CTTGAAATGCA	TTGTGCTAGAT	GCCTTAAGTAT	TGAAAAAGT	289
Db	319	CTAACAAATCA	TAGTAAAGACA	ATTATATTGCT	CTTCCAGGTG	TTATCACAA	2655

```

RESULT 14
US-10-750-623-29889/C
; Sequence 29889, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OR INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750.623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29889
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Bovine 19866881745929
US-10-750-623-29889

```

Query Match	5.3%	Score 34.2	DB 7	Length 601
Best Local Similarity	49.7%	Pred. No. 7.3		
Matches 87; Conservative	0	Mismatches 88	Indels 0	Gaps 0

QY 115 TTCAAGCTTTTAACTATATGTGTGCAATTAAGTTTAAAGTATCATATGAAGGTG 174

Db 439 TTAAAGCTGTTTATTCCTTTGAAAAGATBAGATTTTAACTAAGGAGACTGTGAT 387

QY 175 TGCAGAAGACATGAAGGCAAGATTAACGGATGAAACCATTAAGCTTTGGCTAT 234

Db 379 TCATGCAATTAGAAATTGCATCGAAGAGTACATGCTCTTTTAAAGACTTTGCTATTGT 320

QY 235 CAGACCAATPACTTGAATGACACTGTGTAGCATGCTTAAGTATTGAAGAGT 289

Db 319 CTAAACATCATAGTAAAGACAACTATTATTGCTCTCCAGAGTGTATCACAAGT 265

```

RESULT 15
US-10-750-185-62480
? Sequence 62480, Application US/10750185
? Publication No. US2005026063A1
? GENERAL INFORMATION:
? APPLICANT: MMI GENOMICS, INC.
? APPLICANT: DENISE, Sue K.
? APPLICANT: KERR, Richard
? APPLICANT: ROSENFELD, David
? APPLICANT: HOLM, Tom
? APPLICANT: BATES, Stephen
? APPLICANT: PANTIN, Dennis
? TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
? FILE REFERENCE: MM1100-2
? CURRENT APPLICATION NUMBER: US/10/750,185
? CURRENT FILING DATE: 2003-12-31
? PRIOR APPLICATION NUMBER: US 60/437,482
? PRIOR FILING DATE: 2002-12-31
? NUMBER OF SEQ ID NOS: 64922
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 62480
? LENGTH: 3232
? TYPE: DNA
? ORGANISM: Bovine
? US-10-750-185-62480

```

```

Query Match      5.3%; Score 34.2; DB 7; Length 3232;
Best Local Similarity 52.4%; Pred. No. 11;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 61 ATAAAGCTTGATCTGCAAGTATATATACAGTTAGCTACACAGTTTGTACTTCAG 120
    |||||
Db 2745 ATTATGCTGTACACCTGAACTATATATATATATATCACTATGCTTCAATAAACA 2804
    |||||

Qy 121 TCTTTTAACTATATGTTGGTGCATAAAGATTATGAGTATCCATATGAAGGTGTGCAAG 180
    |||||
Db 2805 CTTTAAATATMAAAATGTGAAGAACAACATGAAATMAAGCACTGGAATTAATATGCA 2864
    |||||

Qy 181 AGAACATGAAGGCAAGATTA 203
    |||||
Db 2865 AGAAAAAAATCCAAACAAAA 2887
    |||||

```

Search completed: February 12, 2006, 00:26:49
 Job time : 410 secs